

Result No.	Query			ID	Description
	Score	Match	Length		
1	722	100.0	142	4	AAb81022 Human pho
2	722	100.0	154	6	ABR44235 Human sec
3	722	100.0	154	6	ABU63125 Human gro
4	682	91.7	142	3	AAb12810 Mouse sec
5	662	91.7	142	4	AAB881021 Murine pho
6	363.5	50.3	124	6	ADa61984 Human 18M
7	360.5	49.9	124	2	AAr10126 Membrane-
8	360.5	49.9	124	2	AAW73562 Human gro
9	360.5	49.9	124	6	ADa61982 Human G72
10	360.5	49.9	124	6	ADa61978 Human G72
11	360.5	49.9	124	6	ABR83569 Human PLA
12	360.5	49.9	144	1	AAp93112 Human inf
13	360.5	49.9	144	1	AAp93363 Human syn
14	360.5	49.9	144	2	AAr25416 PLA3. 1/1
15	360.5	49.9	144	2	AAr63055 Human PLA
16	360.5	49.9	144	6	ABr44233 Human sec
17	360.5	49.9	144	6	ABp96807 Human pho
18	360.5	49.9	144	6	ABu63123 Human gro
19	360.5	49.9	144	7	ABD75501 Prostata
20	360.5	49.9	144	7	ADb63560 Human pro
21	360.5	49.9	164	3	ABd56432 Human pro
22	357.5	48.5	124	6	ADa61983 Human T10
23	348	48.2	125	6	AAr63060 Rat PLA2
24	347	48.1	146	7	ADb63558 Rat Prote
25	341	47.2	146	2	AAw08368 Mouse PLA

CC and the gene encoding it. Inhibitors of phospholipase A2 have
CC antibacterial; immunosuppressive; anti-inflammatory; tranquilizer;
CC vulnery; antiasthmatic; antiallergic; antirheumatic; and antiarthritic
CC activity. The PLA2 protein, gene and an anti-PLA2 antibody are useful in
CC the diagnosis of PLA2 associated diseases e.g. septic shock, adult
CC respiratory distress syndrome, pancreatitis, trauma, bronchial asthma,
CC allergic rhinitis and rheumatoid arthritis. The present sequence
CC represents human PLA2
XX
SQ Sequence 142 AA;

Query Match 100.0%; Score 722; DB 4; Length 142;
Best Local Similarity 100.0%; Pred. No. 8.5e-59;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLVQGVMIKMTGKSALOYNDYCYGIGGSHWVPDQTDWCCHAHDCCYGRLEKLGCEP 60
DB 20 NLVQGVMIKMTGKSALOYNDYCYGIGGSHWVPDQTDWCCHAHDCCYGRLEKLGCEP 79
QY 61 KLEKLFVSVERGIFCAGRTTCORLTCECDKRAALCFRNLTGNRYKVAHPNKLCTGPT 120
DB 80 KLEKLFVSVERGIFCAGRTTCORLTCECDKRAALCFRNLTGNRYKVAHPNKLCTGPT 139
QY 121 PPC 123
DB 140 PPC 142

RESULT 2
ABR44235
ID ABR44235 standard; protein; 154 AA.
XX
AC ABR44235;
XX
DT 18-AUG-2003 (first entry)
XX
DE Human secreted group IIE phospholipase A2 (sPLA2) enzyme.

XX Group IIF secreted phospholipase A2; sPLA2; phosphatidylglycerol; human;
KW phosphatidylcholine; antibacterial; virucide; cytostatic; vasoregic;
KW anti-inflammatory; vulnery; cardiant; chromosome lp35; transgenic;
KW enzyme.
XX
OS Homo sapiens.

XX WO2003033689-A1.

XX 24-APR-2003.

XX 12-OCT-2001; 2001WO-IB002407.

XX 12-OCT-2001; 2001WO-IB002407.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Lazdunski M, Lambeau G, Valentin E;

XX WPI; 2003-403216/38.

XX Novel mammalian secreted group IIF secreted phospholipase A2, useful for
PT preventing and treating bacterial and viral infections, and cancers.

XX Disclosure; Fig 1; 33pp; English.

XX The invention relates to a mammalian secreted group IIF secreted
CC phospholipase A2 (sPLA2) (1), where the enzyme is Ca2+ dependent,
CC maximally active at pH 7-8 and hydrolyzes phosphatidylglycerol versus
CC phosphatidylcholine with a 15-fold preference. A pharmaceutical
CC composition comprising (1) is useful for treating or preventing viral and
CC bacterial infections, and cancers. A pharmaceutical composition
CC containing compounds capable of inhibiting catalytic activity of (1),
CC biologically active compounds that bind sPLA2 receptors, or a compound
CC that modulates cell proliferation, cell migration, cell contraction or

CC apoptosis is useful for treating disease states or disorders involving
CC group IIF sPLA2, such as inflammatory disease, cancers, cardiac and brain
CC ischaemia, acute lung injury, acute respiratory distress syndrome or
CC Crohn's disease. Specific antibodies are useful for searching new
CC secreted mammalian group IIF sPLA2 or the homologues of the enzyme in
CC other mammals. The encoding polynucleotides and vectors are useful for
CC transforming animals and establishing a line of transgenic animals.
CC Sequences ABR44232-238 represent various human secreted sPLA2 enzymes
CC used in alignment studies with the GIIIF sPLA2 enzyme
XX
SQ Sequence 154 AA;

Query Match 100.0%; Score 722; DB 6; Length 154;
Best Local Similarity 100.0%; Pred. No. 9.1e-59;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLVQGVMIKMTGKSALOYNDYCYGIGGSHWVPDQTDWCCHAHDCCYGRLEKLGCEP 60
DB 32 NLVQGVMIKMTGKSALOYNDYCYGIGGSHWVPDQTDWCCHAHDCCYGRLEKLGCEP 91
QY 61 KLEKLFVSVERGIFCAGRTTCORLTCECDKRAALCFRNLTGNRYKVAHPNKLCTGPT 120
DB 92 KLEKLFVSVERGIFCAGRTTCORLTCECDKRAALCFRNLTGNRYKVAHPNKLCTGPT 151
QY 121 PPC 123
DB 152 PPC 154

RESULT 3
ABU63125
ID ABU63125 standard; protein; 154 AA.

XX ABU63125;

XX 25-SEP-2003 (first entry)

XX Human group IIE secreted phospholipase A2.

XX Human; group IIE secreted phospholipase A2; virucide; antibacterial;
KW cytostatic; anti-inflammatory; vasotropic; cerebroprotective; sPLA2;
KW phosphatidylglycerol hydrolysis; phosphatidylcholine hydrolysis;
KW viral infection; bacterial infection; cancer; inflammatory disease;
KW cardiac ischaemia; brain ischaemia; acute lung injury;
KW acute respiratory distress syndrome; Crohn's disease; enzyme.

XX Homo sapiens.

XX US2003073087-A1.

XX 17-APR-2003.

XX 11-OCT-2001; 2001US-00975456.

XX 11-OCT-2000; 2000US-0239491P.

XX (LAZD/) LAZDUNSKI M.

XX (LAMB/) LAMBEAU G.

XX (VALE/) VALENTIN E.

XX Lazdunski M, Lambeau G, Valentin E;

XX WPI; 2003-567302/53.

XX New mammalian secreted group IIF phospholipase A2 or nucleic acid, useful
PT for treating or preventing viral or bacterial infections, or cancers, or
PT screening inhibitors of the enzyme for treating e.g. inflammatory
PT diseases or ischaemia.

XX Disclosure; Fig 1; 16pp; English.

XX The invention describes a mammalian secreted group IIF phospholipase A2
CC (sPLA2), which is Ca2+-dependent, maximally active at pH of about 7-8,

CC and hydrolyses phosphatidylglycerol versus phosphatidylcholine with about
CC a 15-fold preference. The mammalian secreted group IIF sPLA2 protein or
CC nucleic acid, or a pharmaceutical composition is useful for treating
CC and/or preventing viral infections, bacterial infections, or cancers. The
CC inhibitors of sPLA2 or a composition comprising sPLA2 inhibitors is
CC useful for treating disease states or disorders involving group IIF
CC sPLA2, e.g. inflammatory diseases, cancer, cardiac and brain ischaemia,
CC acute lung injury, acute respiratory distress syndrome, or Crohn's
CC disease. The enzyme is also useful for screening various chemical
CC compounds for treating these diseases. This is the amino acid sequence of
CC human group IIE phospholipase A2 used to determine a consensus sequence
CC for human sPLA2s
XX
SQ Sequence 154 AA;

Query Match 100.0%; Score 722; DB 6; Length 154;
Best Local Similarity 100.0%; Pred. No. 9.1e-59;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NLVQFGWMIKMTGKSAIQYNDYGCYCGIGSGHWPVDQTDWCCHADCCYGRLEKLGCEP 60
Db 32 NLVQFGWMIKMTGKSAIQYNDYGCYCGIGSGHWPVDQTDWCCHADCCYGRLEKLGCEP 91
Qy 61 KLEKLVSVSERGIFCAGRTTCORLTCECDKRAALCFRRNLGTYNRYAHYPNKLCTGPT 120
Db 92 KLEKLVSVSERGIFCAGRTTCORLTCECDKRAALCFRRNLGTYNRYAHYPNKLCTGPT 151
Qy 121 PPC 123
Db 152 PPC 154

RESULT 4
AAB12810
ID AAB12810 standard; protein; 142 AA.
XX
AC AAB12810;
XX
DT 27-NOV-2000 (first entry)
XX
DE Mouse secretory type phospholipase A2 protein SEQ ID NO:15.
XX
KW Mouse; secretory phospholipase A2; PLA2; screening; development;
XX inhibitor.
XX
OS Mus musculus.
XX
PN JP2000166568-A.
XX
PD 20-JUN-2000.
XX
PF 09-DEC-1998; 98JP-00349604.
XX
PR 09-DEC-1998; 98JP-00349604.
XX
PA (SHIO) SHIONOGI & CO LTD.
XX
XX WPI; 2000-485554/43.
DR N-PSDB; AAA73130.
XX
PT New gene encoding mouse secretory type phospholipase A2 (PLA2) for
PT screening for inhibitors of PLA2.
XX
PS Claim 1; Page 13-14; 15pp; Japanese.
XX
CC The present invention describes a mouse secretory type phospholipase A2
CC (PLA2) protein. The mouse secretory type PLA2-like protein can be used
CC for screening in the development of inhibitors against the function of
CC the protein. The present sequence represents mouse secretory type PLA2
XX
SQ Sequence 142 AA;
Query Match 91.7%; Score 662; DB 3; Length 142;

Best Local Similarity 88.6%; Pred. No. 2.8e-53;
Matches 109; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
Qy 1 NLVQFGWMIKMTGKSAIQYNDYGCYCGIGSGHWPVDQTDWCCHADCCYGRLEKLGCEP 60
Db 20 NLVQFGWMIKMTGKSAIQYNDYGCYCGIGSGHWPVDQTDWCCHADCCYGRLEKLGCEP 79
Qy 61 KLEKLVSVSERGIFCAGRTTCORLTCECDKRAALCFRRNLGTYNRYAHYPNKLCTGPT 120
Db 80 KLEKLVSVSERGIFCAGRTTCORLTCECDKRAALCFRRNLGTYNRYAHYPNKLCTGPT 139
Qy 121 PPC 123
Db 140 PPC 142

RESULT 5
AAB81021
ID AAB81021 standard; protein; 142 AA.
XX
AC AAB81021;
XX
DT 12-JUN-2001 (first entry)
XX
DE Marine phospholipase A2 (PLA2) amino acid sequence.
XX
KW Phospholipase A2; PLA2; antibacterial; immunosuppressive; vulnery;
KW antiinflammatory; tranquilliser; antiasthmatic; antiallergic; trauma;
KW antirheumatic; antiarthritic; septic shock; pancreatitis; mouse;
KW adult respiratory distress syndrome; ARDS; bronchial asthma;
KW allergic rhinitis; rheumatoid arthritis.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= Signal_peptide
FT Protein 20..142
FT /label= Mature_PLA2
FT /note= "Mature phospholipase A2"
XX
PN WO200121775-A1.
XX
PD 29-VAR-2001.
XX
PF 18-SEP-2000; 2000WO-JP006344.
XX
PR 21-SEP-1999; 99JP-00266616.
XX
PA (SHIO) SHIONOGI & CO LTD.
XX
PI Ishizaki J, Suzuki N, Hanasaki K;
XX
DR WPI; 2001-290432/30.
DR N-PSDB; AAF77387.
XX
PT Human secretory phospholipase A2 and encoded gene, useful in diagnosis of
PT and screening drug candidates for treating associated diseases e.g.
PT septic shock, adult respiratory distress syndrome and rheumatoid
PT arthritis.
XX
PS Example 3; Page 42; 50pp; Japanese.
XX
CC This invention relates to human secretory phospholipase A2 (PLA2) protein
CC and the gene encoding it. Inhibitors of phospholipase A2 have
CC antibacterial, immunosuppressive; antiinflammatory; tranquilliser;
CC vulnery; antiasthmatic; antiallergic; antirheumatic; and antiarthritic
CC activity. The PLA2 protein, gene and an anti-PLA2 antibody are useful in
CC the diagnosis of PLA2 associated diseases e.g. septic shock, adult
CC respiratory distress syndrome, pancreatitis, trauma, bronchial asthma,
CC allergic rhinitis and rheumatoid arthritis. The present sequence
CC represents murine PLA2. The murine PLA2 gene sequence is used in the
CC invention for the identification and characterisation of the human PLA2

CC Gene
XX Sequence 142 AA;
SQ

Query Match 91.7%; Score 662; DB 4; Length 142;
Best Local Similarity 88.6%; Pred. No. 2.8e-53;
Matches 109; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 NLVQGVMIERMTGKSAIQYNDYCYGICGSHWPVDQTDWCCHADCCYGRLEKLGCEP 60
DB 20 NLVQGVMIERMTGKSAIQYNDYCYGICGSHWPVDQTDWCCHADCCYGRLEKLGCDP 79
QY 61 KLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRNLGTYNRYAHYPNKLCTGPT 120
DB 80 KLEKYLFSITRDNIFCAGRTACORHTCECDKRAALCFRNLGTYNRYAHYPNKLCTGPT 139
QY 121 PPC 123
DB 140 PPC 142

RESULT 6
ADA61984
ID ADA61984 standard; protein; 124 AA.
XX
AC ADA61984;
DT 20-NOV-2003 (first entry)
XX
DE Human I8M/G72K/T103K PLA2 mutant.
XX
KW -Antibacterial; gram-positive bacteria; human; group IIA phospholipase A2;
KW group IIA PLA2; bacterial infection; Staphylococcus aureus;
KW multi-drug resistance; wound; bloodstream infection;
KW methicillin-resistant S. aureus; MRSA; nosocomial infection;
KW vancomycin-resistant Enterococcus faecium; mutagen; mutant.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 8 /note= "Wild-type Ile substituted by Met"
FT Misc-difference 72 /note= "Wild-type Gly substituted by Lys"
FT Misc-difference 103 /note= "Wild-type Thr substituted by Lys"
XX
FN US6475484-B1.
XX
XX 05-NOV-2002.
XX
PF 18-DEC-2000; 2000US-00740569.
XX
PR 17-DEC-1999; 99US-0172467P.
XX
XX (UYNY) UNIV NEW YORK STATE.
XX
XX Weiss J, Elsbach P, Liang N;
XX
DR WPI; 2003-219013/21.
XX
XX Treating a patient suffering from infection caused by gram-positive
XX bacteria or killing gram-positive bacteria, comprises delivering mutant
XX human Group IIA phospholipase A2.
XX
PS Example 1; Page; 22pp; English.
XX
XX The invention relates to killing gram-positive bacteria (I) in human
XX patient, comprising contacting the bacteria with a bactericidal-effective
XX amount of mutant human Group IIA phospholipase A2 (Group IIA PLA2)
XX appearing as ADA61978, or treating a human patient suffering from
XX infection caused by a bacteria comprising administering a mutant human

CC Group IIA PLA2 and an antibiotic. The methods of the invention are useful
CC for killing Gram-positive bacteria, (especially Staphylococcus aureus)
CC and for treating human patient suffering from an infection caused by Gram
CC -positive bacteria. The bacteria are selected from Micrococcus,
CC Staphylococcus, Streptococcus, Peptococcus, Peptostreptococcus,
CC Enterococcus, Methanobacterium, Bacillus, Clostridium, Lactobacillus,
CC Listeria, Erysipelothrix, Corynebacterium, Propionibacterium,
CC Eubacterium, Actinomyces, Arachnia, Bifidobacterium, Bacterionema,
CC Rothia, Mycobacterium, Nocardia, Streptomyces and Micropolyospora. The
CC methods are useful for treating potentially life-threatening infection
CC caused by multi-drug resistant Gram positive bacteria, for treating wound
CC and bloodstream infection with methicillin-resistant S. aureus (MRSA) and
CC nosocomial infections with vancomycin-resistant Enterococcus faecium. The
CC present sequence represents the I8M/G72K/T103K mutant PLA2 of the
CC invention. Note: The present sequence is not shown in the specification
CC but was created by the indexer using the information in example 1 and the
CC sequence appearing as ADA61978.
XX
XX Sequence 124 AA;
SQ

Query Match 50.3%; Score 363.5; DB 6; Length 124;
Best Local Similarity 55.6%; Pred. No. 7.5e-26;
Matches 69; Conservative 10; Mismatches 44; Indels 1; Gaps 1;

QY 1 NLVQGVMIERMTGK-SALQYNDYCYGICGSHWPVDQTDWCCHADCCYGRLEKLGCE 59
DB 1 NLVQGVMIERMTGKSAIQYNDYCYGICGSHWPVDQTDWCCHADCCYGRLEKLGCG 60
QY 60 PKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRNLGTYNRYAHYPNKLCTGP 119
DB 61 TFLSYKFSNSKRITCAQDSRCSQLCEDCAATCFARNKTYNKKYQYYSNKHGRGS 120
QY 120 TPPC 123
DB 121 TPRC 124

RESULT 7
AAR10126
ID AAR10126 standard; protein; 124 AA.
XX
XX AAR10126;
XX
AC AAR10126;
DT 25-MAR-2003 (revised)
DT 19-MAR-1991 (first entry)
XX
XX Membrane-bound phospholipase A2 from human spleen.
XX
XX human phospholipase A2; anti-inflammatory drugs.
XX
XX Homo sapiens.
XX
XX JP02286081-A.
XX
XX 26-NOV-1990.
XX
XX 27-APR-1989; 89JP-00110269.
XX
XX 27-APR-1989; 89JP-00110269.
XX
XX (SHIO) SHIONOGI & CO LTD.
XX
XX WPI; 1991-012217/02.
XX
XX Human spleen deriving membrane bound phospholipase A2 - used for
XX screening antiinflammatory drug.
XX
XX Claim 2; Page 1; 6pp; Japanese.
XX
XX Human spleen was homogenated then centrifuged to obtain a precipitated
XX pellet comprising the cell membrane component. The pellet was extracted
XX with KBr aq. solution. Pure phospholipase A2 was obtained from the crude
XX preparation by a combination of chromatography techniques. The protein

CC can be used as an antigen to generate monoclonal antibodies with
 CC specificity against human spleen- derived phospholipase A2. The
 CC monoclonal antibodies can be used in the diagnosis of inflammation.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 124 AA;

Query Match 49.9%; Score 360.5; DB 2; Length 124;
 Best Local Similarity 55.6%; Pred. No. 1.4e-25;
 Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;
 XX
 SQ Sequence 124 AA;

QY 1 NLVQFGVMIEKMTGK-SALOYNDYGCYGGSHWPVDQDWCCHAHDCYGRLEKLGCE 59
 DB 1 NLVNFHRMILKTGKEAALSYGFYCHGCGVGRGSPKDATDRCCVTHDCCYKRLKRGCG 60
 QY 60 PKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRYAHYPNKLCTGP 119
 DB 61 TKFLSYKFSNSGRITCAKQDCRSQKCECDKAAATCFARNKTTYNNKYQYYSNKHCRGS 120
 QY 120 TPPC 123
 DB 121 TPRC 124

RESULT 8
 AA073562
 ID AA073562 standard; protein; 124 AA.
 XX
 AC AA073562;

DT 10-MAR-1999 (first entry)

DE Human group II secretory phospholipase A2 protein.

XX Human group II secretory phospholipase A2; hspLA2 grII; Fxa inhibitor;
 KW coagulation disorder; haemostatic disorder; Fva/Fva complex formation;
 KW therapy.
 XX

OS Homo sapiens.

PN WO9855504-A1.

PD 10-DEC-1998.

PF 04-JUN-1998; 98WO-IB000869.

PR 05-JUN-1997; 97US-0048668P.

PA (INSP) INST PASTEUR.

PI Mounier C, Hackeng T, Griffin J, Bon C;

DR WPI; 1999-045729/04.

XX New peptide fragment of human group II secretory phospholipase A2 (hsPLA2
 PT grII) - useful in the treatment or prevention of coagulation and
 PT hemostatic disorders.
 XX

PS Example 6; Page 27; 62pp; English.

XX This sequence represents the full length human group II secretory
 CC phospholipase A2 (hsPLA2 grII) protein. The invention relates to peptides
 CC comprising eleven amino acids, corresponding to residues 51-62 of hsPLA2
 CC grII. The peptides are useful in screening new compounds for their
 CC potential use as drugs in the treatment or prevention of coagulation
 CC disorders (particularly thrombus formation and limiting platelet
 CC activation in vivo in humans and animals). The peptides and antibodies
 CC form compositions in the regulation of the coagulant effect in vivo in
 CC humans or animals. The peptides are also useful, in forming kits in the
 CC detection of haemostatic disorders. Additionally, the peptides and
 CC antibodies form compositions in the treatment or prevention of
 CC haemostatic disorders. The peptide represents the specific region of
 CC hsPLA2 grII involved in the inhibition of the Fva/Fva complex formation,

CC and Fxa inhibition, which maximizes the effects of drugs based on the
 CC peptide
 XX
 SQ Sequence 124 AA;

Query Match 49.9%; Score 360.5; DB 2; Length 124;
 Best Local Similarity 55.6%; Pred. No. 1.4e-25;
 Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;
 XX
 SQ Sequence 124 AA;

QY 1 NLVQFGVMIEKMTGK-SALOYNDYGCYGGSHWPVDQDWCCHAHDCYGRLEKLGCE 59
 DB 1 NLVNFHRMILKTGKEAALSYGFYCHGCGVGRGSPKDATDRCCVTHDCCYKRLKRGCG 60
 QY 60 PKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRYAHYPNKLCTGP 119
 DB 61 TKFLSYKFSNSGRITCAKQDCRSQKCECDKAAATCFARNKTTYNNKYQYYSNKHCRGS 120
 QY 120 TPPC 123
 DB 121 TPRC 124

RESULT 9

ADA61982

ID ADA61982 standard; protein; 124 AA.

XX
 AC ADA61982;

DT 20-NOV-2003 (first entry)

DE Human G72K PLA2 mutant.

XX Antibacterial; gram-positive bacteria; human; group IIA phospholipase A2;

KW group IIA PLA2; bacterial infection; Staphylococcus aureus;
 KW multi-drug resistance; wound; bloodstream infection;
 KW methicillin-resistant S. aureus; MRSA; nosocomial infection;
 KW vancomycin-resistant Enterococcus faecium; murein; mutant.

OS Synthetic.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Misc-difference 72

FT /note= "Wild-type Gly substituted by Lys"

XX US6475484-B1.

XX 05-NOV-2002.

XX 18-DEC-2000; 2000US-00740569.

XX 17-DEC-1999; 99US-0172467P.

XX (UJNY) UNIV NEW YORK STATE.

XX Weiss J, Elsbach P, Liang N;

XX WPI; 2003-219013/21.

XX Treating a patient suffering from infection caused by gram-positive
 PT bacteria or killing gram-positive bacteria, comprises delivering mutant
 PT human Group IIA phospholipase A2.
 XX

XX Example 1; Page; 22pp; English.

XX The invention relates to killing gram-positive bacteria (I) in human
 CC patient, comprising contacting the bacteria with a bactericidal-effective
 CC amount of mutant human Group IIA phospholipase A2 (Group IIA PLA2)
 CC appearing as ADA61978, or treating a human patient suffering from
 CC infection caused by a bacteria comprising administering a mutant human
 CC Group IIA PLA2 and an antibiotic. The methods of the invention are useful
 CC for killing Gram-positive bacteria, (especially Staphylococcus aureus)
 CC and for treating human patient suffering from an infection caused by Gram

CC -positive bacteria. The bacteria are selected from Micrococcus,
 CC Staphylococcus, Streptococcus, Peptococcus, Peptostreptococcus,
 CC Enterococcus, Methanobacterium, Bacillus, Clostridium, Lactobacillus,
 CC Listeria, Erysipelothrix, Corynebacterium, Propionibacterium,
 CC Eubacterium, Actinomyces, Arachnia, Bifidobacterium, Bacterionema, The
 CC Rothia, Mycobacterium, Nocardia, Streptomyces and Micropolytopora. The
 CC methods are useful for treating potentially life-threatening infection
 CC caused by multi-drug resistant Gram positive bacteria, for treating wound
 CC and bloodstream infection with methicillin-resistant S. aureus (MRSA) and
 CC nosocomial infections with vancomycin-resistant Enterococcus faecium. The
 CC present sequence represents the G72K mutant PLA2 of the invention. Note:
 CC the present sequence is not shown in the specification but was created by
 CC the indexer using the information in example 1 and the sequence appearing
 CC as ADA61978.
 XX
 SQ Sequence 124 AA;
 Query Match 49.9%; Score 360.5; DB 6; Length 124;
 Best Local Similarity 54.8%; Pred. No. 1.4e-25;
 Matches 68; Conservative 11; Mismatches 44; Indels 1; Gaps 1;
 QY 1 NLVQFGVMIEKMTGK-SALQYNDYGCYGGGSHWPDQTDWCCHADCCYGRLEKLGCE 59
 Db 1 NLVNFHRLIKLTGKEAALSYGFYCHGCGVGRGSPKDATDRCCVTHDCCKYKLEKRGCG 60
 QY 60 PKLEKYLFSVSEIRGIFCAGRTTCORLTCECDKRAALCFRRNLGTYNRYKHAHPNKLCTGP 119
 Db 61 TKFLSYKFSNSKRITCAKQDSCRSQLECDKAAATCFARNKTYNKKYQYVSNHCRGS 120
 QY 120 TPPC 123
 Db 121 TPRC 124
 RESULT 10
 ADA61978
 ID *ADA61978 standard; protein; 124 AA.
 AC ADA61978;
 XX 20-NOV-2003 (first entry)
 DT Human G72K/Ti03K PLA2 mutant.
 DE
 XX Antibacterial; gram-positive bacteria; human; group IIA phospholipase A2;
 KW group IIA PLA2; bacterial infection; Staphylococcus aureus;
 KW multi-drug resistance; wound; bloodstream infection;
 KW methicillin-resistant S. aureus; MRSA; nosocomial infection;
 KW vancomycin-resistant Enterococcus faecium; muten; mutant.
 XX Synthetic.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Key
 FT Misc-difference 72
 FT /note= "Wild-type Gly substituted by Lys"
 FT Misc-difference 103
 FT /note= "Wild-type Thr substituted by Lys"
 FT
 FN US6475484-B1.
 XX
 XX 05-NOV-2002.
 PD
 XX 18-DEC-2000; 2000US-00740569.
 PF
 XX 17-DEC-1999; 95US-0172467P.
 PR
 XX (UNYX) UNIV NEW YORK STATE.
 PA Weiss J, Elsbach P, Liang N;
 XX WPI; 2003-219013/21.
 DR N-PSDB; ADA61977.
 XX

XX Treating a patient suffering from infection caused by gram-positive
 PT bacteria or killing gram-positive bacteria, comprises delivering mutant
 PT human Group IIA phospholipase A2.
 XX Claim 1; Fig 3; 22pp; English.
 PS
 XX The invention relates to killing gram-positive bacteria (I) in human
 CC patient, comprising contacting the bacteria with a bactericidal-effective
 CC amount of mutant human Group IIA phospholipase A2 (Group IIA PLA2)
 CC appearing as ADA61978, or treating a human patient suffering from
 CC infection caused by a bacteria comprising administering a mutant human
 CC Group IIA PLA2 and an antibiotic. The methods of the invention are useful
 CC for killing gram-positive bacteria, (especially Staphylococcus aureus)
 CC and for treating human patient suffering from an infection caused by Gram
 CC -positive bacteria. The bacteria are selected from Micrococcus,
 CC Staphylococcus, Streptococcus, Peptococcus, Peptostreptococcus,
 CC Enterococcus, Methanobacterium, Bacillus, Clostridium, Lactobacillus,
 CC Listeria, Erysipelothrix, Corynebacterium, Propionibacterium,
 CC Eubacterium, Actinomyces, Arachnia, Bifidobacterium, Bacterionema,
 CC Rothia, Mycobacterium, Nocardia, Streptomyces and Micropolytopora. The
 CC methods are useful for treating potentially life-threatening infection
 CC caused by multi-drug resistant Gram positive bacteria, for treating wound
 CC and bloodstream infection with methicillin-resistant S. aureus (MRSA) and
 CC nosocomial infections with vancomycin-resistant Enterococcus faecium. The
 CC present sequence represents the G72K/Ti03K mutant PLA2 of the invention.
 XX
 SQ Sequence 124 AA;
 Query Match 49.9%; Score 360.5; DB 6; Length 124;
 Best Local Similarity 54.8%; Pred. No. 1.4e-25;
 Matches 68; Conservative 11; Mismatches 44; Indels 1; Gaps 1;
 QY 1 NLVQFGVMIEKMTGK-SALQYNDYGCYGGGSHWPDQTDWCCHADCCYGRLEKLGCE 59
 Db 1 NLVNFHRLIKLTGKEAALSYGFYCHGCGVGRGSPKDATDRCCVTHDCCKYKLEKRGCG 60
 QY 60 PKLEKYLFSVSEIRGIFCAGRTTCORLTCECDKRAALCFRRNLGTYNRYKHAHPNKLCTGP 119
 Db 61 TKFLSYKFSNSKRITCAKQDSCRSQLECDKAAATCFARNKTYNKKYQYVSNHCRGS 120
 QY 120 TPPC 123
 Db 121 TPRC 124
 RESULT 11
 ABR83569
 ID ABR83569 standard; protein; 124 AA.
 XX
 AC ABR83569;
 XX 14-OCT-2003 (first entry)
 DT Human PLA2 amino acid sequence SEQ ID NO:36.
 XX Fusion protein; TolA; TolAIII domain; ber; Escherichia coli; human;
 KW interaction; cleavage site.
 XX Homo sapiens.
 OS
 XX WO2003057708-A2.
 PN
 XX 17-JUL-2003.
 PD
 XX 10-JAN-2003; 2003WO-GB0000078.
 PF
 XX 10-JAN-2002; 2002GB-00000689.
 PR
 XX (UYNE-) UNIV NEWCASTLE VENTURES LTD.
 PA Gokce I, Anderlueh G, Lakey JH;
 XX

DR WPI; 2003-587105/55.
XX New fusion polypeptides, useful for immobilization or purification and
XX isolation of the non-Tola polypeptide, or for studying interaction
PT properties of the non-Tola polypeptide or the fusion polypeptide, e.g.
PT self-interaction.
XX
XX
PS Example 1; Page 56-57; 68pp; English.
XX
XX The present invention describes a fusion polypeptide (I) for expression
XX in a host cell comprising a TolAII domain (functional homologue,
XX fragment or derivative), and a non-Tola polypeptide, where the TolAII
XX domain (functional homologue, fragment or derivative) is located towards
XX the N-terminus of the fusion polypeptide, and the non-Tola polypeptide is
XX located towards the C-terminus of the fusion polypeptide. Also described:
XX (1) a DNA molecule (II) encoding the fusion polypeptide (I); (2) an
XX expression vector (III) comprising the fusion polypeptide (I); (3) a
XX cloning vector (IV) for producing the expression vector comprising DNA
XX (II) encoding the TolAII domain (functional homologue, fragment or
XX derivative) upstream or downstream from a cloning site which allows in-
XX frame insertion of DNA encoding a non-Tola polypeptide; and (4) a host
XX cell containing (II), and/or (III), and/or (IV). The TolAII domain
XX (functional homologue, fragment or derivative) is useful for producing
XX the fusion polypeptide (I), DNA molecule (II), expression vector (III) or
XX cloning vector (IV). The fusion polypeptide (I) is useful for
XX immobilization or purification and isolation of the non-Tola polypeptide,
XX or for studying interaction properties of the non-Tola polypeptide or the
XX fusion polypeptide, e.g. self-interaction, interaction with another
XX molecule or interaction with a physical stimulus and for high expression
XX of a polypeptide as a fusion polypeptide in a host cell. ACF57145 to
XX ACF57176 and ABR83541 to ABR83574 represent sequence used in the
XX exemplification of the present invention
XX
XX Sequence 124 AA;
XX
XX Query Match 49.9%; Score 360.5; DB 6; Length 124;
XX Best Local Similarity 55.6%; Pred. No. 1.4e-25;
XX Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;
XX
QY 1 NLVQFGVMIEKMTGK-SALQYNDYGCYGGIGGSHWPVDQTDWCCHADCCYGRLEKLGCE 59
Db 1 NLVNFHFMILKLTGKEALSYGFYGCYGGVGRGSPKDATDRCCVTHDCCYKLEKRGCG 60
QY 60 PKLEKYLFSVSEKIFCAGRTTCORLTCECDKRAALCFERNLCTYKRYAHYPNKLCGTGP 119
Db 61 TKELSYKFSNSGRITCAKQDSRCSQLCECDKRAALCFARNKTYKRYAHYPNKLCGTGP 120
QY 120 TPCC 123
Db 121 TPRC 124
XX
XX
XX RESULT 12
XX ADP93112
XX ID AAP93112 standard; protein; 144 AA.
XX AC AAP93112;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 31-JUL-1992 (first entry)
XX XX
XX Human inflammatory phospholipase A2 encoded by HindIII fragment of PLA2
XX 8.5 EMBL3.
XX
XX Inflammation; acid stable; phosphatide 2-acylhydrolase; lipolytic;
KW glycerophospholipids; non-pancreatic.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH 1..20
XX FT Peptide /label= signal
XX FT /label= exon_1
XX FT Region 1..14

FT Region /label= exon_1
FT 15..62
FT /label= exon_2
FT 21..39
FT /note= "Claim 12"
FT 22..37
FT /note= "Claim 14"
FT 44..56
FT /note= "calcium binding loop"
FT 63..98
FT /label= exon_3
FT 67
FT Active-site
FT Binding-site
FT 68
FT /note= "calcium binding"
FT 71
FT Active-site
FT 86
FT Active-site
FT 99..124
FT /label= exon_4
FT 111
FT Active-site
XX
XX WO8909818-A.
XX
XX 19-OCT-1989.
XX
XX 11-APR-1989; 89WO-US001418.
XX
XX 15-APR-1988; 88US-00181893.
XX 12-JUL-1988; 88US-00219491.
XX
XX (BIOJ) BIOGEN INC.
XX
XX Kramer RM, Pepinsky R, Hession C;
XX
XX WPI; 1989-324225/44.
XX N-PSDB; AAN91825, AAN97209.
XX
XX Acid stable phospholipase A2 - used for prodn. of antibodies and in the
XX treatment or diagnosis of inflammation and other diseases.
XX
XX Claim 44; Fig 12; 84pp; English.
XX
XX The protein sequence was deduced from a DNA sequence obtd. from a genomic
XX DNA library which was prep'd. from a mutant fibroblast cell line which
XX contains 5 copies of the X chromosome (GMS009). The signal sequence is
XX thought to be incomplete at the N-terminal since no promoter-like
XX sequences are found in the DNA within 100 nucleo- tides 5' of this
XX region. The deduced N-terminal sequence of the mature protein confirmed
XX results obtd. by direct sequencing of the purified protein. This sequence
XX represents an amphiphilic alpha-helix typical of PLA 2 mols. It has
XX highly conserved lipophilic residues [e.g. Leu (22), Phe (25), and Ile
XX (29)] and there is a cluster of basic amino acids [e.g. Arg (27), Lys
XX (30) and Lys (35)] which is believed to be an important determinant in
XX the interaction of PLA 2. There is a characteristic stretch of residues
XX which comprises part of the calcium binding loop: Tyr(44)-Gly-X-Cys-
XX Gly-X-Gly-X-X-X-Pro(56) and Asp(58). The conserved residues which
XX constitute the active site (see features) are also present, and the
XX protein exhibits the placement of half-cysteine residues typical of a Gp
XX II PLA 2, having a Cys residue at position 70 and a half cysteine at the
XX C-terminal. (The consensus sequence was determined from a comparison of
XX PLA 2s from bovine pancreas and C. atrox venom. (Updated on 25-MAR-2003
XX to correct PR field.)
XX
XX Sequence 144 AA;
XX
XX Query Match 49.9%; Score 360.5; DB 1; Length 144;
XX Best Local Similarity 55.6%; Pred. No. 1.6e-25;
XX Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;
XX
QY 1 NLVQFGVMIEKMTGK-SALQYNDYGCYGGIGGSHWPVDQTDWCCHADCCYGRLEKLGCE 59
Db 21 NLVNFHFMILKLTGKEALSYGFYGCYGGVGRGSPKDATDRCCVTHDCCYKLEKRGCG 80
QY 60 PKLEKYLFSVSEKIFCAGRTTCORLTCECDKRAALCFERNLCTYKRYAHYPNKLCGTGP 119

Db 81 TKFLSYKFSNSGSRITCAKQDSCRSQSCDCAAAATCFARNKTTYNKKYQYYSNKHCRGS 140
 QY 120 TPPC 123
 Db 141 TPRC 144

RESULT 13
 AAP93363
 ID AAP93363 standard; protein; 144 AA.
 XX AC AAP93363;
 XX 25-MAR-2003 (revised)
 DT 27-JUN-1980 (first entry)
 DE Human synovial phospholipase type A2 (sPLA2) as encoded by cDNA clone
 DE lambda SPLA2cDNA-4 and by the exons of clone lambda SPLA2-6.
 XX Human synovial phospholipase A2; clone lambda SPLA2cDNA-4;
 KW lambda SPLA2-6.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FT Protein 21..144
 XX WO901773-A.
 XX 09-MAR-1989.
 XX 23-AUG-1988; 88WO-US002896.
 XX 27-AUG-1987; 87US-00089883.
 PR 06-JUL-1988; 88US-00215726.
 PR -16-AUG-1988; 88US-00231865.
 XX (BIOT-) BIOTECHN RES PARTN.
 PA (UTOR) UNIV OF TORONTO INNOVAT.
 XX Johnson LK, Seilhamer JJ, Pruzanski W, Vadas P;
 WPI; 1989-085394/11.
 DR N-PSDB; AAN91258, AAN91260.
 XX Mammalian synovial phospholipase A2 - used in food processing, design and
 FT screening of inflammation inhibitors, as an anticancer drug or vaccine
 FT adjuvant etc.
 XX Disclosure; Fig 6; 70pp; English.
 PS
 CC Clone lambda SPLA2cDNA-4 is one of four clones identified when probe
 CC oligo 2905 (AAN91257) was used to screen a cDNA library constructed from
 CC polyA+ message from a peritoneal cell RNA. It encodes the entire sPLA2
 CC type A sequence which is given here. The mature peptide sequence (see FT)
 CC has a calculated molecular weight of 13,919 daltons. The same amino acid
 CC sequence is also encoded by the exons of clone lambda SPLA2-6 (AAN91260)
 CC in Figure 7. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25
 CC -MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI
 CC field.)
 XX Sequence 144 AA;
 SQ
 Query Match 49.9%; Score 360.5; DB 1; Length 144;
 Best Local Similarity 55.6%; Pred. No. 1.6e-25;
 Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;
 QY 1 NLVQFVMIKXGK-SALQYNDYCYGIGGSHWPVDQTDWCHAHDCCYGRLEKGC 59
 Db 21 NLVNFHRIKLTGTGKEAALSYGFYCHGCVGRGSPKDATDRCCVTHDCCYKLEKGC 80
 QY 60 PKLEYLFSVSEGRIFCAGRTTCQRLTCECDKRAALCFERNLGTYNRYAHYPNKLCTGP 119

Db 81 TKFLSYKFSNSGSRITCAKQDSCRSQSCDCAAAATCFARNKTTYNKKYQYYSNKHCRGS 140
 QY 120 TPPC 123
 Db 141 TPRC 144

RESULT 14
 AAR25416
 ID AAR25416 standard; protein; 144 AA.
 XX AC AAR25416;
 XX 06-JAN-1993 (first entry)
 DT PLA2.
 DE Human growth hormone; granulocyte-colony stimulating factor; G-CSF;
 KW phospholipase A2; HGH; PCR; polymerase chain reaction; gene therapy;
 KW erythroid cells; cDNA library.
 XX Synthetic.
 OS
 XX GB2251622-A.
 XX 15-JUL-1992.
 XX 19-DEC-1991; 91GB-00026984.
 XX 21-DEC-1990; 90GB-00027917.
 XX (ICIL) IMPERIAL CHEM IND PLC.
 XX Hollis M, Needham MRC, Gooding C, Grosveld FG, Antoniou M;
 WPI; 1992-236158/29.
 DR N-PSDB; AAR26372.
 XX Expression vectors for use in mammalian cells - contain dominant control
 PT region derived from beta-globin gene.
 XX Disclosure; Fig 11; 77pp; English.
 CC This sequence is encoded by the phospholipase A2 (PLA2) cDNA. The cDNA
 CC was amplified using the primer sequences given in AAR26370-1 by PCR from
 CC a human lung cDNA library. The cDNA sequence was used in the construction
 CC of an expression vector which further comprised a promoter and a dominant
 CC control region. This vector was used in an expression system comprising a
 CC mammalian cell transformed with the vector. This expression system could
 CC be used to prepare pharmacologically useful polypeptides eg. human growth
 CC hormone (HGH), granulocyte-colony stimulating factor (G-CSF) and PLA2,
 CC and for gene therapy. The mammalian host comprises erythroid cells and a
 CC heterologous promoter
 XX Sequence 144 AA;
 SQ
 Query Match 49.9%; Score 360.5; DB 2; Length 144;
 Best Local Similarity 55.6%; Pred. No. 1.6e-25;
 Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;
 QY 1 NLVQFVMIKXGK-SALQYNDYCYGIGGSHWPVDQTDWCHAHDCCYGRLEKGC 59
 Db 21 NLVNFHRIKLTGTGKEAALSYGFYCHGCVGRGSPKDATDRCCVTHDCCYKLEKGC 80
 QY 60 PKLEYLFSVSEGRIFCAGRTTCQRLTCECDKRAALCFERNLGTYNRYAHYPNKLCTGP 119
 Db 81 TKFLSYKFSNSGSRITCAKQDSCRSQSCDCAAAATCFARNKTTYNKKYQYYSNKHCRGS 140
 QY 120 TPPC 123
 Db 141 TPRC 144

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OM protein - protein search, using sw model

Run on: July 3, 2004, 05:17:51 ; Search time 43.6302 Seconds
(without alignments)
877.555 Million cell updates/sec

Title: US-10-088-092a-30_COPY_20_142

Perfect score: 722

Sequence: 1 NLVQFGVMIEKWTGKSLQY.....YNRKYAHYPNKLCTGTPPC 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 31123816 residues

Total number of hits satisfying chosen parameters: 1276540

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	722	100.0	154	10	US-09-975-456B-8
2	360.5	49.9	124	14	US-10-255-576-2
3	360.5	49.9	144	10	US-09-975-456B-6
4	360.5	49.9	144	14	US-10-205-823-325
5	360.5	49.9	144	15	US-10-116-275-269
6	360.5	49.9	164	9	US-09-925-300-1010
7	341	47.2	146	9	US-09-993-999-8
8	341	47.2	146	13	US-10-124-591-3
9	337	46.7	146	13	US-10-124-591-4
10	335.5	46.5	138	12	US-09-917-805-7
11	330.5	45.8	138	12	US-09-917-805-6
12	311.5	43.1	138	12	US-09-917-805-2
13	303	42.0	168	10	US-09-975-456B-2
14	303	42.0	168	15	US-10-104-047-3735
15	303	42.0	211	14	US-10-345-680-23

16	303	42.0	211	15	US-10-295-027-195	Sequence 195, Appl
17	303	42.0	211	16	US-10-278-938-2	Sequence 2, Appli
18	303	42.0	211	16	US-10-188-832-80	Sequence 80, Appl
19	299.5	41.5	118	9	US-09-987-655-5	Sequence 5, Appli
20	299.5	41.5	118	9	US-09-987-675-5	Sequence 5, Appli
21	299.5	41.5	138	10	US-09-975-456B-9	Sequence 9, Appli
22	292.5	40.5	145	9	US-09-969-384-17	Sequence 17, Appli
23	292.5	40.5	145	10	US-09-975-456B-7	Sequence 7, Appli
24	290.5	40.2	145	9	US-09-835-968A-6	Sequence 6, Appli
25	290.5	40.2	150	12	US-10-296-115-1342	Sequence 1342, Ap
26	288.5	40.0	137	9	US-09-993-999-9	Sequence 9, Appli
27	287.5	39.8	135	10	US-09-975-456B-10	Sequence 10, Appl
28	287.5	39.8	165	13	US-10-124-591-1	Sequence 1, Appli
29	270.5	37.5	145	12	US-09-917-805-9	Sequence 9, Appli
30	265	36.7	145	12	US-09-917-805-4	Sequence 4, Appli
31	249	34.5	145	12	US-09-917-805-5	Sequence 5, Appli
32	227.5	31.5	145	12	US-09-917-805-8	Sequence 8, Appli
33	226.5	31.4	148	10	US-09-975-456B-5	Sequence 5, Appli
34	226.5	31.4	148	12	US-09-917-805-3	Sequence 3, Appli
35	226.5	31.4	156	9	US-09-925-297-511	Sequence 511, App
36	225.5	31.2	146	12	US-09-917-805-1	Sequence 1, Appli
37	216	29.9	146	9	US-09-993-999-7	Sequence 7, Appli
38	200	27.7	151	12	US-10-398-663-7	Sequence 7, Appli
39	198.5	27.5	152	14	US-10-230-058A-15	Sequence 15, Appl
40	193.5	26.8	133	15	US-10-371-725-7	Sequence 7, Appli
41	186	25.8	143	9	US-09-993-999-10	Sequence 10, Appl
42	178	24.7	153	15	US-10-369-493-5548	Sequence 5548, Ap
43	175	24.2	116	10	US-09-946-374-378	Sequence 378, App
44	175	24.2	116	12	US-10-147-493-534	Sequence 534, App
45	175	24.2	116	12	US-10-145-127-534	Sequence 534, App

ALIGNMENTS

RESULT 1

US-09-975-456B-8
; Sequence 8, Application US/09975456B
; Publication NO. US20030073087A1
; GENERAL INFORMATION:
; APPLICANT: LAZDUNSKI, MICHEL
; APPLICANT: LAMBEAU, GERARD
; APPLICANT: VALENTIN, EMMANUEL
; TITLE OF INVENTION: NOVEL MAMMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2
; FILE REFERENCE: 1478-R-00
; CURRENT APPLICATION NUMBER: US/09/975,456B
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/239,491
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 2.1
; SEQ ID NO 8
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-975-456B-8

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						Gaps	0
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Db	32	NLVQFGVMIEKWTGKSLQYNDYCYCGIGGSHWPVQTDWCCHADCCYGRLEKLGCEP	91				
Qy	61	KLEKXVLSVSRGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRYAHYPNKLCTGPT	120				
Db	92	KLEKXVLSVSRGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRYAHYPNKLCTGPT	151				
Qy	121	PPC 123					
Db	152	PPC 154					

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RESULT 2
US-10-255-576-2
; Sequence 2, Application US/10255576
; Publication No. US20030161822A1
; GENERAL INFORMATION:
; APPLICANT: Weiss, Jerrold
; APPLICANT: Elsbach, Peter
; APPLICANT: Liang, Ning-Sheng
; TITLE OF INVENTION: ANTIBACTERIAL GROUP IIA PHOSPHOLIPASE A2 AND METHODS OF USE THERE
; FILE REFERENCE: 5986/1E917U51
; CURRENT APPLICATION NUMBER: US/10/255,576
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US/09/740,569
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/172,467
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-255-576-2
Query Match 49.9%; Score 360.5; DB 14; Length 124;
Best Local Similarity 54.8%; Pred. No. 5.8e-32;
Matches 68; Conservative 11; Mismatches 44; Indels 1; Gaps 1;
QY 1 NLVQFGVMIEKMTGK-SALQYNDYGCYIGGSHWFPVDQTDWCCHADCCVGRLEKLGCE 59
DB 1 NLVNFHRLIKLTTGKEAALSFGYCHGCGVGRGSPKDATDRCCVTHDCCYKRLKRGCG 60
QY 60 PKLEKYLFSVSRGIFCAGRTTCQRLTCECDRAALCFRRNLGTYNRYKHYHPNKLCTGP 119
DB 61 TKFLSYKFSNSKSRITCAKQDSCRSQLCECDKAAATCFARNKTTYNNKYQYYSNKHCRGS 120
QY 120 TPPC 123
DB 121 TPRC 124
RESULT 3
US-09-975-456B-6
; Sequence 6, Application US/09975456B
; Publication No. US20030073087A1
; GENERAL INFORMATION:
; APPLICANT: LAZDUNSKI, MICHEL
; APPLICANT: LAMBEAU, GERARD
; APPLICANT: VALENTIN, EMMANUEL
; TITLE OF INVENTION: NOVEL MAMMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2
; FILE REFERENCE: 1478-R-00
; CURRENT APPLICATION NUMBER: US/09/975,456B
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/239,491
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in version 2.1
; SEQ ID NO 6
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-975-456B-6
Query Match 49.9%; Score 360.5; DB 10; Length 144;
Best Local Similarity 55.6%; Pred. No. 6.8e-32;
Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;
QY 1 NLVQFGVMIEKMTGK-SALQYNDYGCYIGGSHWFPVDQTDWCCHADCCVGRLEKLGCE 59
DB 21 NLVNFHRLIKLTTGKEAALSFGYCHGCGVGRGSPKDATDRCCVTHDCCYKRLKRGCG 80
QY 60 PKLEKYLFSVSRGIFCAGRTTCQRLTCECDRAALCFRRNLGTYNRYKHYHPNKLCTGP 119
DB 61 TKFLSYKFSNSKSRITCAKQDSCRSQLCECDKAAATCFARNKTTYNNKYQYYSNKHCRGS 140
RESULT 4
US-10-205-823-325
; Sequence 325, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Monsey, Argela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 325
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-325
Query Match 49.9%; Score 360.5; DB 14; Length 144;
Best Local Similarity 55.6%; Pred. No. 6.8e-32;
Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;
QY 1 NLVQFGVMIEKMTGK-SALQYNDYGCYIGGSHWFPVDQTDWCCHADCCVGRLEKLGCE 59
DB 21 NLVNFHRLIKLTTGKEAALSFGYCHGCGVGRGSPKDATDRCCVTHDCCYKRLKRGCG 80
QY 60 PKLEKYLFSVSRGIFCAGRTTCQRLTCECDRAALCFRRNLGTYNRYKHYHPNKLCTGP 119
DB 81 TKFLSYKFSNSKSRITCAKQDSCRSQLCECDKAAATCFARNKTTYNNKYQYYSNKHCRGS 140
QY 120 TPPC 123
DB 141 TPRC 144
RESULT 5
US-10-116-275-269
; Sequence 269, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
```



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1  RESULT 8
2  US-10-124-591-3
3  / Sequence 3, Application US/10124591
4  / Publication No. US20020177208A1
5  / GENERAL INFORMATION:
6  / APPLICANT: Hawkins, Phillip R.
7  / Bardman, Olga
8  / Quegler, Karl J.
9  / Shah, Purvi
10 / Corley, Neil C.
11 /
12 / TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
13 /
14 / NUMBER OF SEQUENCES: 4
15 / CORRESPONDENCE ADDRESS:
16 / ADDRESSER: Incyte Pharmaceuticals, Inc.
17 / STREET: 3174 Porter Dr.
18 / CITY: Palo Alto
19 / STATE: CA
20 / COUNTRY: USA
21 / ZIP: 94304
22 /
23 / COMPUTER READABLE FORM:
24 / MEDIUM TYPE: Diskette
25 / COMPUTER: IBM Compatible
26 / OPERATING SYSTEM: DOS
27 /
28 / SOFTWARE: FastSeq for Windows Version 2.0
29 /
30 / CURRENT APPLICATION DATA:
31 / APPLICATION NUMBER: US/10/124,591
32 / FILING DATE: 16-Apr-2002
33 /
34 / PRIOR APPLICATION DATA:
35 / APPLICATION NUMBER: US/09/489,770
36 / FILING DATE: <Unknown>
37 / APPLICATION NUMBER: 08/966,317
38 / FILING DATE: <Unknown>

```

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0403 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 984837
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-124-591-3
Query Match 47.2%; Score 341; DB 13; Length 146;
Best Local Similarity 52.8%; Pred. No. 9.9e-30;
Matches 66; Conservative 9; Mismatches 48; Indels 2; Gaps 2;
QY 1 NLVQGVMIKMTGKSA-LQYNDYCYGCGIGGSHWPVDQTDWCCHADCCVGRLEKLGCE 59
Db 22 NLVQGVMIKMTGKSA-LQYNDYCYGCGIGGSHWPVDQTDWCCHADCCVGRLEKLGCE 81
QY 60 PKLEKYLFSVSRGIFCA-GRITTCORLTCCDRAALCFRRNLGTYNRYKHYAHYPNKLTCTG 118
Db 82 TKLLKYKSHOGGQITCSANQNSCKRLCQCDKAAECFARNKKTYSLKTYQFYNNMFCG 141
QY 119 PTPPC 123
Db 142 KKPXC 146
RESULT 9
US-10-124-591-4
Sequence 4, Application US/10124591
Publication No. US20020177208A1
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
Bandman, Olga
Guebler, Karl J.
Shah, Purvi
Corley, Neil C.
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,591
FILING DATE: 16-Apr-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/489,770
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/966,317
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0403 US
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 204319
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-124-591-4
Query Match 46.7%; Score 337; DB 13; Length 146;
Best Local Similarity 50.4%; Pred. No. 2.8e-29;
Matches 63; Conservative 14; Mismatches 46; Indels 2; Gaps 2;
QY 1 NLVQGVMIKMTGKSA-LQYNDYCYGCGIGGSHWPVDQTDWCCHADCCVGRLEKLGCE 59
Db 22 SLLEFGQMLFKTKRADVSFYGCHGCGVGRGSPKDATDWCCTHDCVNRLEKGGC 81
QY 60 PKLEKYLFSVSRGIFCA-GRITTCORLTCCDRAALCFRRNLGTYNRYKHYAHYPNKLTCTG 118
Db 82 TKLLKYKSHOGGQITCSANQNSCKRLCQCDKAAECFARNKKTYSLKTYQFYNNMFCG 141
QY 119 PTPPC 123
Db 142 KKPXC 146
RESULT 10
US-09-917-805-7
Sequence 7, Application US/09917805
Publication No. US2004007937A1
GENERAL INFORMATION:
APPLICANT: STYME, Sten
APPLICANT: STAHL, Ulf
APPLICANT: EK, Bo
APPLICANT: SJODAHL, Staffan
TITLE OF INVENTION: PLANT ENZYME AND USE THEREOF
FILE REFERENCE: STYME-1
CURRENT APPLICATION NUMBER: US/09/917,805
PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 09/155,124
PRIOR FILING DATE: 1999-03-02
PRIOR APPLICATION NUMBER: PCT/SE97/00554
PRIOR FILING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: 9601237.2
PRIOR FILING DATE: 1996-03-29
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 7
LENGTH: 138
TYPE: PRT
ORGANISM: Bothrops jararacussu
US-09-917-805-7
Query Match 46.5%; Score 335.5; DB 12; Length 138;
Best Local Similarity 50.0%; Pred. No. 3.8e-29;
Matches 62; Conservative 12; Mismatches 47; Indels 3; Gaps 2;
QY 1 NLVQGVMIKMTGKSA-LQYNDYCYGCGIGGSHWPVDQTDWCCHADCCVGRLEKLGCE 59
Db 17 DLWQFGQMLFKTKRADVSFYGCHGCGVGRGSPKDATDWCCTHDCVNRLEKGGC 74
QY 60 PKLEKYLFSVSRGIFCA-GRITTCORLTCCDRAALCFRRNLGTYNRYKHYAHYPNKLTCTG 119
Db 75 PKTDYRYSRENGVIICGEGTPECEQICECDKAAECFARNKKTYSLKTYQFYNNMFCG 134
QY 120 TTPC 123
Db 135 AEKC 138

Query Match 43.1%; Score 311.5; DB 12; Length 138;
Best Local Similarity 50.8%; Pred. No. 1.7e-26;
Matches 63; Conservative 12; Mismatches 44; Indels 5; Gaps 4

Qy	2	LVQGVMIKTKT	GSALQYNDYCYCGIGSFWPQTDQWCHADCCYGRLEKLGCEP	60
Db	18	LMQFENMIKVK	SGILSVSAYCYCGWGRGPKDADRCCFVHDCYGVK--TGCNP	75
Qy	61	KLEKLVFSVSRGIF	CAGRITTCORLTCCECDKRAALCFRRNLGTYNR-KYAHYPNKLCTGP	119
Db	76	KLGGTYTSWNGND	IVCEGDGFCEV-CECDRAAICFRNLDTYDRNKWRYPASNCQED	134
Qy	120	TPPC	123	
		:		
Db	135	SEPQ	138	

RESULT 13
US-09-975-456B-2
; Sequence 2, Application US/09975456B
; Publication No. US20030073087A1
; GENERAL INFORMATION:
; APPLICANT: LAZDUNSKI, MICHEL
; APPLICANT: LAMBEAU, GERARD
; APPLICANT: VALENTIN, EMMANUEL
; TITLE OF INVENTION: NOVEL MANUALLIAN SECRETED GROUP IIF PHOSPHOLIPASE A2
; FILE REFERENCE: 1478-R-00
; CURRENT APPLICATION NUMBER: US/09/975,456B
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/239,491
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin version 2.1
; SEQ ID NO 2
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-975-456B-2

Query Match	42.0%;	Score 303;	DB 10;	Length 168;
Best Local Similarity	43.3%;	Pred. No. 1.9e-25;		
Matches	55;	Conservative	18;	Mismatches 48;
				Indels 6;
				Gaps 4

[illegible]

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RESULT 14
US-10-104-047-3735
; Sequence 3735, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 3735
; LENGTH: 168
; TYPE: PRT

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RESULT 11
US-09-917-805-6
; Sequence 6, Application US/09917805
; Publication No. US20040073973A1
; GENERAL INFORMATION:
; APPLICANT: STYMNE, Sten
; APPLICANT: STAHL, Ulf
; APPLICANT: EK, Bo
; APPLICANT: SJODAHL, Staffan
; TITLE OF INVENTION: PLANT ENZYME AND USE THEREOF
; FILE REFERENCE: STYMNE-1
; CURRENT APPLICATION NUMBER: US/09/917,805
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 09/155,124
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: PCT/SE97/00554
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: 9601237.2
; PRIOR FILING DATE: 1996-03-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Vipera ammodytes
US-09-917-805-6

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Query Match	45.8%;	Score 330.5;	DB 12;	Length 138;
Best Local Similarity	47.6%;	Pred. No. 1.4e-28;		
Matches 59; Conservative	18;	Mismatches 44;	Indels 3;	Gaps 2;
QY	1	NLVQFGVMIEKMTGKSAL-OYNDVGYCYGGIGSHWPVDQTDCWCHAHDDCCYGRLEKLGCSE	59	
		::::: :: :		
Db	17	SLLEFGMMLIGETGNPLTSYFYCGYCGVGKGTPKDATRCCFVHCDCCGNLP--DCS	74	
		::: :: :		
QY	60	PKELYLFSVSERGFICAGRTTCORLICEDCKRAALCFRRNLGTYNRYKHAYHPNKLCTGP	119	
		::: :: :		
Db	75	PKTDRYKHRENGAIVCGKGTSGENRICEDRAAAIFCRKNLTNYIYRNPDPFLCKCE	134	
		::: :: :		

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RESULT 12
US-09-917-805-2
; Sequence 2, Application US/09917805
; Publication No. US20040073973A1
; GENERAL INFORMATION:
; APPLICANT: STYMNE, Sten
; APPLICANT: STAHL, Ulf
; APPLICANT: EK, Bo
; APPLICANT: SOODAHL, Staffan
; TITLE OF INVENTION: PLANT ENZYME AND USE THEREOF
; FILE REFERENCE: STYMNE=1
; CURRENT APPLICATION NUMBER: US/09/917,805
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 09/155,124
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: PCT/SE97/00554
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: 9601237.2
; PRIOR FILING DATE: 1996-03-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 2
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Trimeresurus flavoviridis
US-09-917-805-2

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ORGANISM: Homo sapiens
US-10-104-047-3735
Query Match 42.0%; Score 303; DB 15; Length 168;
Best Local Similarity 43.3%; Pred. No. 1.9e-25;
Matches 55; Conservative 18; Mismatches 48; Indels 6; Gaps 4;
Search completed: July 3, 2004, 05:27:05
Job time : 43.6302 secs

QY 1 NLVQFGVMIEKMTGKSA-LQVNDYGCYCGIGGSHWPDQTDWCHAHDCCYGRLEKLGCE 59
DB 21 SLNLKAMVEAVTGRSAILSFGVGYCGYGLGGRGQPKDEVDWCHAHDCCYQELFDGCH 80
QY 60 PKLEKYLFSV-SERGIICA--GRTTCORLTCECDKRAALCFRRNLGTYNKRYAHYFNKLC 116
DB 81 PYVDHYDHTIENNTIIVCSDLNKTCDKQTCMCDKNNVLCIMNQ--TYREYRGLNLYC 138
QY 117 TGTPTPC 123
DB 139 QGTPNC 145

RESULT 15
US-10-345-680-23
; Sequence 23, Application US/10345680
; Publication No. US20030148394A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 12327, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MPI02-012PIRNM.OMNI
; CURRENT APPLICATION NUMBER: US/10345,680
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-345-680-23

Query Match 42.0%; Score 303; DB 14; Length 211;
Best Local Similarity 43.3%; Pred. No. 2.4e-25;
Matches 55; Conservative 18; Mismatches 48; Indels 6; Gaps 4;
QY 1 NLVQFGVMIEKMTGKSA-LQVNDYGCYCGIGGSHWPDQTDWCHAHDCCYGRLEKLGCE 59
DB 64 SLNLKAMVEAVTGRSAILSFGVGYCGYGLGGRGQPKDEVDWCHAHDCCYQELFDGCH 123
QY 60 PKLEKYLFSV-SERGIICA--GRTTCORLTCECDKRAALCFRRNLGTYNKRYAHYFNKLC 116
DB 124 PYVDHYDHTIENNTIIVCSDLNKTCDKQTCMCDKNNVLCIMNQ--TYREYRGLNLYC 181

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 3, 2004, 05:13:08 ; Search time 25.9925 Seconds
(without alignments)
1493.077 Million cell updates/sec

Title: US-10-088-092A-30_COPY_20_142

Perfect score: 722

Sequence: 1 NLVDFGVMIKXWTKSALQY.....YNRKHYHFNKLTGTPPTPC 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phase:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacteriap:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	349	48.3	146	11	Q91Y34
2	333.5	46.2	138	13	Q7T1D5
3	325.5	45.1	138	13	Q805A3
4	323.5	44.8	138	13	Q8AXY1
5	322.5	44.8	138	13	Q805A2
6	315.5	43.7	138	13	Q7ZTA8
7	314.5	43.6	138	13	Q7ZTA6
8	313.5	43.4	138	13	Q7T1D1
9	312.5	43.3	138	13	Q7T1D4
10	312.5	43.3	138	13	Q7T1D3
11	312.5	43.3	138	13	Q7T1D2
12	310.5	43.0	138	13	Q800C1
13	309.5	42.9	138	13	Q800C2
14	309.5	42.9	138	13	Q7ZTA7
15	305.5	42.3	138	13	Q800C4
16	303	42.0	168	4	Q8N217

ALIGNMENTS

RESULT 1

Q91Y34
ID Q91Y34 PRELIMINARY; PRT; 146 AA.
AC Q91Y34;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Platelet phospholipase A2 precursor (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=wislar; TISSUE=Blood;
RA Liu T.T., Liang N.S., Meng Z.Q., Xie Y.A., Kuang Z.P., Li Y.;
RT "Cloning and sequence determination of rat platelet phospholipase A2
from whole blood";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF365363; AAK52061.1;
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00568; phoslip; 1.
DR PRINTS; PR00389; PHEHLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2C; 1.
DR PROSITE; PS00119; PA2_ASP; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
KW Signal.
FT SIGNAL. 1 21
FT CHAIN 22 >146
FT NON_TER 146 146
SQ SEQUENCE 146 AA; 16306 MW; 60C1C9EC85DCBD67 CRC64;

POTENTIAL.
PLATELET PHOSPHOLIPASE A2.

Query Match 48.3%; Score 349; DB 11; Length 146;
Best Local Similarity 51.2%; Pred.No. 3.1e-33;
Matches 64; Conservative 14; Mismatches 45; Indels 2; Gaps 2;

Q7T2R1 vipera russ
Q800C3 crotalus vi
Q8CE14 mus musculu
Q8T3T5 vipera russ
Q8N435 homo sapien
Q7Z3Q1 vipera russ
Q7T3S7 echis carin
Q804D7 bothrops ja
Q8K0Y1 mus musculu
Q8J93 mus musculu
Q7C1C6 vipera aspi
Q8C5Y6 mus musculu
Q9QX68 mesocricetu
Q8AY48 bungarus ca
Q8AXW0 bungarus mu
Q8AXW1 bungarus mu
Q7L1R0 bungarus fl
Q7Z60 rana catesb
Q8AXW2 bungarus mu
Q7L1R1 bungarus fl
Q9DEB0 pagrus majo
Q8AXW7 micrurus co
Q8XW8 adamsia car
Q7C2Q4 bungarus fl
Q80211 bungarus ca
Q9U8P8 asterina pe
Q7C2Q5 bungarus fl
Q9YH62 dicentrarch
Q9U8P9 asterina pe

QY 1 NLVQFGVMEKMTGSA-LOVNDYGCYGGSHWPDQTDWCHADCCYGRLEKLGCE 59
DB 22 SLLEFGQMIFPKTKRADVSFGYGCYGGSHWPDQTDWCHADCCYGRLEKLGCE 81
QY 60 PKLEKYLFSVSEGRIFCA-GRITTCORLTCECDKRAALCFRRNLGTNNRYAHYFNKLCTG 118
DB 82 TKFTYFVSRRGHSISTWQDSCKQLCCDRAAEFCFARNKKSYSCLKYQFYPNFKCG 141
QY 119 TTPPC 123
DB 142 KTPSC 146
RESULT 2
Q7TID5 PRELIMINARY; PRT; 138 AA.
AC Q7TID5;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Phospholipase A2.
GN PLA2VB.
OS Vipera berus (Common viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Vipera.
OX NCBI_TaxID=31156;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22707820; PubMed=12823540;
RX Guillemin L., Bouchier C., Garrigues T., Wisner A., Choumet V.;
RT "Sequences and structural organization of phospholipase A2 genes from
RT Vipera aspis aspis, V. aspis zinnikeri and Vipera berus venom.
RT Identification of the origin of a new viper population based on
RT amodyrin II heterogeneity."
RL Eur. J. Biochem. 270:2697-2706(2003).
DR EMBL; AY158636; AAN59982.1; -.
SQ SEQUENCE 138 AA; 15716 MW; 79B9F9E0D16C9CBB CRC64;
Query Match 46.2%; Score 333.5; DB 13; Length 138;
Best Local Similarity 48.4%; Pred. No. 2e-31;
Matches 60; Conservative 14; Mismatches 47; Indels 3; Gaps 2;
QY 1 NLVQFGVMEKMTGSA-LOVNDYGCYGGSHWPDQTDWCHADCCYGRLEKLGCE 59
DB 17 NLVQFGVMEKMTGSA-LOVNDYGCYGGSHWPDQTDWCHADCCYGRLEKLGCE 74
QY 60 PKLEKYLFSVSEGRIFCA-GRITTCORLTCECDKRAALCFRRNLGTNNRYAHYFNKLCTGP 119
DB 75 PKLSTYSYFQNGNIVCGNKYGLCECDRAAEFCFARNKKSYSCLKYQFYPNFKCG 134
QY 120 TTPC 123
DB 135 SDKC 138
RESULT 3
Q805A3 PRELIMINARY; PRT; 138 AA.
AC Q805A3;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Phospholipase A2.
GN PLA-N.
OS Trimeresurus flavoviridis (Habu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=88087;
RN [1]
RP SEQUENCE FROM N.A.

RA Chijiwa T., Hamai S., Tsubouchi S., Ogawa T., Deshimaru M.,
RA Oda-Ueda N., Hattori S., Kihara H., Tsunazawa S., Ohno M.;
RT "Interisland mutation of a novel phospholipase A2 from Trimeresurus
RT flavoviridis venom and evolution of crotalinae group II phospholipase
RT A2."
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB102728; BAC56892.1; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PR00389; PHEHLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2c; 1.
DR PROSITE; PS00119; PA2_ASP; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
SQ SEQUENCE 138 AA; 15817 MW; A2F7B5A23897ECCS CRC64;
Query Match 45.1%; Score 325.5; DB 13; Length 138;
Best Local Similarity 49.2%; Pred. No. 1.8e-30;
Matches 61; Conservative 13; Mismatches 47; Indels 3; Gaps 2;
QY 1 NLVQFGVMEKMTGSA-LOVNDYGCYGGSHWPDQTDWCHADCCYGRLEKLGCE 59
DB 17 NLVQFGVMEKMTGSA-LOVNDYGCYGGSHWPDQTDWCHADCCYGRLEKLGCE 74
QY 60 PKLEKYLFSVSEGRIFCA-GRITTCORLTCECDKRAALCFRRNLGTNNRYAHYFNKLCTGP 119
DB 75 PKSDIYSYSWKTGVIICGEGTECEKQICECDRAAEFCFARNKKSYSCLKYQFYPNFKCTDP 134
QY 120 TTPC 123
DB 135 TEKC 138
RESULT 4
Q8AXY1 PRELIMINARY; PRT; 138 AA.
AC Q8AXY1;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypotensive phospholipase A2.
OS Bothrops jararacussu (Jararacussu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8726;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=22157211; PubMed=12167491;
RA Andrao-Escarcos S.H., Soares A.M., Fontes M.R., Fuly A.L.,
RA Correa F.M., Rosa J.C., Greene L.J., Giglio J.R.;
RT "Structural and functional characterization of an acidic platelet
RT aggregation inhibitor and hypotensive phospholipase A(2) from Bothrops
RT jararacussu snake venom."
RL Biochem. Pharmacol. 64:723-732(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX Roberto P.G., Kashima S., Soares A.M., Astolfi-Filho S., Giglio J.R.,
RA Franca S.C.;
RT "Functional and Structural Analysis of Acidic and Basic Phospholipases
RT A2 from Bothrops jararacussu Snake Venom."
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY145836; AAN37410.1; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.

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DR PRINTS; PR00389; PHPLIPASEA2.
DR ProDom; P000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2C; 1.
DR PROSITE; PS00119; PA2_ASP; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
SQ SEQUENCE 138 AA; 15456 MW; 513647907BFDF04E CRC64;

Query Match 44.8%; Score 323.5; DB 13; Length 138;
Best Local Similarity 46.8%; Pred. No. 3e-30;
Matches 58; Conservative 16; Mismatches 47; Indels 3; Gaps 2;

QY 1 NLVQFGVMIKMTGKS-ALQYNDYGCYCGIGSGHPVDQTDWCCCHADCCYGRLEKLGCE 59
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
B 17 SLWQFGKINVMGESGVQLVSLGCGIGSGQPTDTRCCFVHDCCVGKY--TGCD 74
QY 60 PKLEKYLFSVSRGIFCAGRTTCORLTCECDKRAALCFRNLTGTYNRYKHYHPNKLCTGP 119
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
B 75 PKIDSYTSKNGDVGCGDDPCKKQICECDRVATTCFRDNKDYDIKYNFYGAKNCQEK 134
QY 120 TPPC 123
D 135 SEPC 138

RESULT 5
Q805A2 PRELIMINARY; PRT; 138 AA.
AC Q805A2
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE PLA-N(O).
OS Trimeresurus flavoviridis (Habu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=88087;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56b;
RX MEDLINE=22510024; PubMed=12623078;
RA Tsai I.-H., Wang Y.-M., Chen Y.-H., Tu A.T.;
RT "Geographic variations, cloning, and functional analyses of the venom
RL Arch. Biochem. Biophys. 411:289-296(2003).
DR EMBL; AV120875; AAM80563.1;
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PR00389; PHPLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2C; 1.
DR PROSITE; PS00119; PA2_ASP; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
SQ SEQUENCE 138 AA; 15414 MW; 44A35EA1FE6A39D0 CRC64;

Query Match 43.7%; Score 315.5; DB 13; Length 138;
Best Local Similarity 46.0%; Pred. No. 2.7e-29;
Matches 57; Conservative 16; Mismatches 48; Indels 3; Gaps 2;

QY 1 NLVQFGVMIKMTGKSA-LQYNDYGCYCGIGSGHPVDTWCCCHADCCYGRLEKLGCE 59
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
B 17 NLVQPELLIMTKVAKRSGLLSYSGYCGWGGHGRPDATDRCCFVHDCCVGKY--TDCN 74
QY 60 PKLEKYLFSVSRGIFCAGRTTCORLTCECDKRAALCFRNLTGTYNRYKHYHPNKLCTGP 119
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B 75 PKTASYTSENGEIVCGDDPCKKQVCECDRVAACFRDNIPSYDNKYIOFFAKNCQEK 134
QY 120 TPPC 123
D 135 PEPC 138

RESULT 7
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AC Q7ZTA6;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Acidic phospholipase A2.
OS Crotalus viridis viridis (Prairie rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Crotalus.
OX NCBI_TaxID=8742;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E6b;
RX MEDLINE=22510024; PubMed=12623078;
RA Tsai I.-H., Wang Y.-M., Chen Y.-H., Tu A.T.;
RT "Geographic variations, cloning, and functional analyses of the venom

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Query Match	43.3%	Score	312.5	DB 13	Length	138			
Best Local Similarity	47.6%	Pred.	No. 6.le-29						
Matches	59	Conservative	12	Mismatches	50	Indels	3	Gaps	2

QY	1	NLVQFGVMIEKMTG-KSALQVNDYGCYCGIGGSHWPVDQTDWCCHADHCCVGRLEKLGCE	59
DB	17	HLQFGDMINKTIGIFGMSYIYGCYCGWGGKGPLDATDRCQFVHDCVGRVN--GCD	74
QY	60	PKELYLFSVSRGIFCAGRTTCORLTCECDKRAALCFRRNLGTYNKRYAHYPNKLTGTP	119
DB	75	PKLSTYSFENGDIVCGDDPCLRAVCECDRVAALCFGENMNTYDKKLYMLSLDDKEE	134
QY	120	TPPC 123	
DB	135	SEQC 138	

RESULT 12			
Q800C1	PRELIMINARY;	PRT;	138 AA.
ID	Q800C1		
AC	Q800C1;		
DT	01-JUN-2003 (TtEMBLrel. 24, Created)		
DT	01-JUN-2003 (TtEMBLrel. 24, Last sequence update)		
DT	01-OCT-2003 (TtEMBLrel. 25, Last annotation update)		
DE	Phospholipase A2.		
OS	Crotalus viridis viridis (Prairie rattlesnake).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;		
OC	Viperidae; Crotalinae; Crotalus.		
OX	NCBI_TaxID=8742;		
RN	[1]		
RP	SEQUENCE FROM N.A.		

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DR PRINTS; PRO0389; PHPHLIPASEA2.
DR PrDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2c; 1.
DR PROSITE; PS00119; PA2 ASP; 1.
DR PROSITE; PS00118; PA2 HIS; 1.
SQ SEQUENCE 138 AA; 15556 MW; 09134B8AB3EE3723 CRC64;

Query Match 42.9%; Score 309.5; DB 13; Length 138;
Best Local Similarity 46.0%; Pred. No. 1.4e-28;
Matches 57; Conservative 14; Mismatches 50; Indels 3; Gaps 2

Qy 1 NLVQFGVMIEKMTGKSAI-QYNDYCYGICGGSHWPVDQTDWCCHADCCYGRLEKLGCE 59
Db 17 SLVQFEMMIKVAKSSGLFWYGAYCYGCGWGQGRPDATDRCCFVHDCCYGK--ATDCN 74
Qy 60 PKLEKYLFSVSRGIFPCAGRTTCQRLTCECDKRAALCFRRNLGTYNKRYAHYFNKLCITGP 119
Db 75 PKTASYTYSENGEIVCGDDPCKKQVCECDRAVAACFRDNIPTDYNDKNYRFPFPCQEBE 134

Qy 120 TPFC 123
Db 135 PEFC 138

RESULT 14
Q7ZTA7 PRELIMINARY; PRT; 138 AA.
AC Q7ZTA7
DT 01-JUN-2003 (TEMBLrel. 24, Created)
DT 01-JUN-2003 (TEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Acidic phospholipase A2.
OS Crotalus viridis viridis (Prairie rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Crotalus.
OX NCBI_Taxid=8742;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6D;
RX MEDLINE=22510024; PubMed=12623078;
RA Tsai I.-H.; Wang Y.-M.; Chen Y.-H.; Tu A.T.;
RT Geographic variations, cloning, and functional analyses of the venom
RT acid phospholipases A2 of Crotalus viridis viridis.";
RL Arch. Biochem. Biophys. 411:289-296(2003).
DR EMBL; AV120876; AAM80564.1; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PRO0389; PHPHLIPASEA2.
DR PrDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2c; 1.
DR PROSITE; PS00119; PA2 ASP; 1.
DR PROSITE; PS00118; PA2 HIS; 1.
SQ SEQUENCE 138 AA; 15549 MW; 04FF6D7266D80BFE CRC64;

Query Match 42.9%; Score 309.5; DB 13; Length 138;
Best Local Similarity 45.2%; Pred. No. 1.4e-28;
Matches 56; Conservative 17; Mismatches 48; Indels 3; Gaps 2

Qy 1 NLVQFGVMIEKMTGKSAI-QYNDYCYGICGGSHWPVDQTDWCCHADCCYGRLEKLGCE 59
Db 17 SLVQFEMMIKVAKSSGLFSYSAICYGCGWGQGRPDATDRCCFVHDCCYGK--TDCN 74
Qy 60 PKLEKYLFSVSRGIFPCAGRTTCQRLTCECDKRAALCFRRNLGTYNKRYAHYFNKLCITGP 119
Db 75 PKTASYTYSENGEIVCGDDPCKKQVCECDRAVAACFRDNIPTDYNDKNYRFPFPCQEBE 134

Qy 120 TPFC 123
Db 135 PEFC 138

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 3, 2004, 05:15:00 ; Search time 14.4679 Seconds
(without alignments)
506.699 Million cell updates/sec

Title: US-10-088-092A-30

Perfect score: 817

Sequence: 1 MKSPHVLVFLCLLVALVTGN.....YNRKYAHYPNKLGTGTPPC 142

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	368.5	45.1	144	1	US-08-186-895-10
2	368.5	45.1	144	2	US-08-888-497-37
3	368.5	45.1	144	4	US-09-362-230-37
4	368.5	45.1	144	5	PCT-US94-07926-37
5	360.5	44.1	124	1	US-08-170-360-4
6	360.5	44.1	124	2	US-08-888-497-39
7	360.5	44.1	124	4	US-09-362-230-39
8	360.5	44.1	124	4	US-09-740-569-2
9	360.5	44.1	124	5	PCT-US94-07926-39
10	360.5	44.1	146	2	US-08-888-497-35
11	360.5	44.1	146	4	US-09-362-230-35
12	360.5	44.1	146	5	PCT-US94-07926-35
13	350	42.8	146	3	US-08-966-317-3
14	350	42.8	146	4	US-09-489-770-3
15	349.5	42.8	146	3	US-08-966-317-4
16	349.5	42.8	146	4	US-09-489-770-4
17	348	42.6	125	2	US-08-888-497-42
18	348	42.6	125	4	US-09-362-230-42
19	348	42.6	125	5	PCT-US94-07926-42
20	321	39.3	125	1	US-08-170-360-5
21	317.5	38.9	138	2	US-08-888-497-32
22	317.5	38.9	138	4	US-09-362-230-32
23	317.5	38.9	138	5	PCT-US94-07926-32
24	314.5	38.5	137	2	US-08-888-497-30
25	314.5	38.5	137	4	US-09-362-230-30
26	314.5	38.5	137	5	PCT-US94-07926-30
27	299.5	36.7	118	2	US-08-888-497-40

Sequence 5, Appli
Sequence 40, Appl
Sequence 40, Appl
Sequence 1, Appli
Sequence 44, Appl
Sequence 44, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 43, Appl
Sequence 43, Appl
Sequence 4, Appli
Sequence 34, Appl
Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-08-186-895-10
; Sequence 10, Application US/08186895
; Patent No. 5538885
; GENERAL INFORMATION:
; APPLICANT: Hollis, Melvyn
; APPLICANT: Needham, Maurice R.C.
; APPLICANT: Gooding, Clare
; APPLICANT: Grosveld, Franklin G.
; TITLE OF INVENTION: Expression Systems
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Cushman, Darby & Cushman
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,895
; FILING DATE: 27-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/046,383
; FILING DATE: 09-APR-1993
; APPLICATION NUMBER: US/07/810,414
; ATTORNEY/AGENT INFORMATION:
; NAME: Kokulis, Paul N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: PNK/3893/93802/MJW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 144 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-186-895-10

Query Match 45.1%; Score 368.5; DB 1; Length 144;
Best Local Similarity 52.1%; Pred. No. 5.1e-32;
Matches 73; Conservative 12; Mismatches 46; Indels 9; Gaps 2;


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RESULT 4
PCT-US94-07926-37
; Sequence 37, Application PC/TUS9407926
; GENERAL INFORMATION:
; APPLICANT: Tishfield, Jeffrey J.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07926
; FILING DATE: 15-JUL-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/097,354
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 144 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-07926-37

Query Match 45.1%; Score 368.5; DB 5; Length 144;
Best Local Similarity 52.1%; Pred. No. 5.1e-32;
Matches 73; Conservative 12; Mismatches 46; Indels 9; Gaps 2;

QY 12 LLVALVT-----GNLVQGVMIKMTGK-SALQYNDYGCYGGSHWPDQTDWCC 62
Db 5 LLLAVIMIFGLQAHGNLVNFMHMKLTGKKAALSFGYGCYGGVGRGSPKDATDRCC 64
QY 63 HAHDCYGRLEKLGCSFKLEKLYPSVSRGIFCAGRTTCORLTCECDKRAALCFRNLGT 122
Db 65 VTHDCCYKRLKRGCGTKFLSYKFSNSGRITCAKQDSCRSQLCECDKAAATCFARNKTT 124
QY 123 YNRKYAHYPNKLCTGPTPPC 142
Db 125 YNKYQYYSNKHCRGSTPRC 144

RESULT 5
US-08-170-360-4
; Sequence 4, Application US/08170360
; Patent No. 5656602
; GENERAL INFORMATION:
; APPLICANT: Tseng, Albert P. S.
; APPLICANT: Inglis, Adam
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; TITLE OF INVENTION: PLA2 INHIBITORY COMPOUNDS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/170,360
; FILING DATE: 03-MAR-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PCT/AU92/00333
; FILING DATE: 06-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PK 7058
; FILING DATE: 04-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Ernst, Barbara G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1871-104A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; US-08-170-360-4

Query Match 44.1%; Score 360.5; DB 1; Length 124;
Best Local Similarity 55.6%; Pred. No. 3.1e-31;
Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;

QY 20 NLVQGVMIKMTGK-SALQYNDYGCYGGSHWPDQTDWCCAHDCYGRLEKLGCE 78
Db 1 NLVNFHMKLTGKKAALSFGYGCYGGVGRGSPKDATDRCCVTHDCCYKRLKRGCG 60
QY 79 PKLEKLYPSVSRGIFCAGRTTCORLTCECDKRAALCFRNLGTYNRYAHYPNKLCTGP 138
Db 61 TKFLSYKFSNSGRITCAKQDSCRSQLCECDKAAATCFARNKTTYNKKYQYYSNKHCRGS 120
QY 139 TTPC 142
Db 121 TPRC 124

RESULT 6
US-08-888-497-39
; Sequence 39, Application US/08888497
; Patent No. 5972677
; GENERAL INFORMATION:
; APPLICANT: Tishfield, Jay A.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
ADDRESS: Russell PA
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
STATE: FL
COUNTRY: USA
ZIP: 33301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/888,497
APPLICATION NUMBER: US/08/888,497

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/651,405
FILING DATE:
APPLICATION NUMBER: US/08/097,354
FILING DATE: 26-JUL-1993

ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996

INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-888-497-39

Query Match 44.1%; Score 360.5; DB 2; Length 124;
Best Local Similarity 55.6%; Pred. No. 3.1e-31;
Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;
QY 20 NLVQFVMIKTK-SALQNDYCYGCGSHWPVDQTDWCHADCCYGRLEKLGCE 78
DB 1 NLVNFHRMIKLTGTGKEAALSYGFYCHGCGVGRGSPKDATDRCCVTHDCCYKLEKRGCG 60

QY 79 PKLEKYLFSVSERGIFCAGRTTCORLTCECDKRAALCFRNLTGYNRYAHYPNKLCTGP 138
DB 61 TKFLSYKFSNSGSRITCAKQDSRSQLCECDKAAATCFARNKTYNNKYQYYSNKHCRGS 120

QY 139 TPPC 142
DB 121 TPRC 124

RESULT 7

US-09-362-230-39
Sequence 39, Application US/09362230
Patent No. 6352849

GENERAL INFORMATION:

APPLICANT: Tishfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
ADDRESS: Russell PA
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
STATE: FL
COUNTRY: USA

ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/09/362,230
APPLICATION NUMBER: US/09/362,230

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/888,497
FILING DATE:
APPLICATION NUMBER: US/08/097,354
FILING DATE: 26-JUL-1993

ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996

INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-362-230-39

Query Match 44.1%; Score 360.5; DB 4; Length 124;
Best Local Similarity 55.6%; Pred. No. 3.1e-31;
Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;
QY 20 NLVQFVMIKTK-SALQNDYCYGCGSHWPVDQTDWCHADCCYGRLEKLGCE 78
DB 1 NLVNFHRMIKLTGTGKEAALSYGFYCHGCGVGRGSPKDATDRCCVTHDCCYKLEKRGCG 60

QY 79 PKLEKYLFSVSERGIFCAGRTTCORLTCECDKRAALCFRNLTGYNRYAHYPNKLCTGP 138
DB 61 TKFLSYKFSNSGSRITCAKQDSRSQLCECDKAAATCFARNKTYNNKYQYYSNKHCRGS 120

QY 139 TPPC 142
DB 121 TPRC 124

RESULT 8

US-09-740-569-2
Sequence 2, Application US/09740569
Patent No. 6475484

GENERAL INFORMATION:

APPLICANT: Weiss, Jerrold
APPLICANT: Liang, Ning-Sheng
TITLE OF INVENTION: ANTIBACTERIAL GROUP IIA PHOSPHOLIPASE A2 AND METHODS OF USE THEREK
FILE REFERENCE: 5986/1E917US1
CURRENT APPLICATION NUMBER: US/09/740,569
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US 60/172,467
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 124
TYPE: PRT
ORGANISM: Homo sapiens

US-09-740-569-2
Query Match 44.1%; Score 360.5; DB 4; Length 124;
Best Local Similarity 54.8%; Pred. No. 3.1e-31;
Matches 68; Conservative 11; Mismatches 44; Indels 1; Gaps 1;

Qy	20	NLVQGVGMIETKGTG-SALQYNDYCYCGIGSGSHWPVDQTDWCCHAHDCCYGRLEKLGCE	78
Db	1	NLVNPHRLIKLTGKEALSYGFYGHGCVGRGSPKDATDRCCVTHDCCYKLEKRGCG	60
Qy	79	PKLEYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRKYAHYPNKLCTGP	138
Db	61	TKFLGYKFNSKSRITCAQDSQSCRSQLECDKAAATCFARNKTYNKKQYVYNKTCRGS	120
Qy	139	TPPC	142
Db	121	TPRC	124

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RESULT 9
PCT-US94-07926-39
; Sequence 39, Application PC/TUS9407926
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSER: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07926
; FILING DATE: 15-JUL-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/097,354
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-07926-39

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Qy      139  TPPC 142
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Db      121  TPRC 124

RESULT 10
US-08-888-497-35
/ Sequence 35, Application US/08888497
/ Patent No. 5972677
/ GENERAL INFORMATION:
/ APPLICANT: Tischfield, Jay A.
/ APPLICANT: Seilhamer, Jeffrey J.
/ TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
/ TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
/ TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
/ TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
/ TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
/ NUMBER OF SEQUENCES: 44
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
/ ADDRESSEE: Russell PA
/ STREET: 200 East Broward Boulevard
/ CITY: Fort Lauderdale
/ STATE: FL
/ COUNTRY: USA
/ ZIP: 33301
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/888,497
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/651,405
/ FILING DATE:
/ APPLICATION NUMBER: US 08/097,354
/ FILING DATE: 26-JUL-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Manso, Peter J.
/ REGISTRATION NUMBER: 32,264
/ REFERENCE/DOCKET NUMBER: IN21044-5
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 305-527-2498
/ TELEFAX: 305-764-4996
/ INFORMATION FOR SEQ ID NO: 35:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 146 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-888-497-35

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RESULT 11


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/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/966,317
/ FILING DATE: Filed Herewith
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0403 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-855-0555
/ TELEFAX: 650-845-4166
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 146 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GenBank
/ CLONE: 984837
/ US-08-966-317-3

Query Match 42.8%; Score 350; DB 3; Length 146;
Best Local Similarity 53.1%; Pred. No. 4.9e-30;
Matches 68; Conservative 9; Mismatches 49; Indels 2; Gaps 2;

QY 17 VTGNLVQFGVMIEKMTGKSA-LQYNDYGCYGGSHWPDVDTWCCHAHDCCYGRLEKL 75
DB 19 VQGNIAQFGEMIRLTKGRAELSYAFYGHGGLGGSPKDATDRCCVTHDCCYKSLKS 78

QY 76 GCEPKLEKYLFSVSRGIFC-AGRTTCORLTCECDKRAALCFRRNLGTYNRYAHYPNKL 134
DB 79 GCGTKLLKYKSHQGQITCSANQNSCQRLCQCDKAAAECPARNKKTYSLKYYQFYPNMF 138

QY 135 CTGPTPPC 142
DB 139 CKGKKPKC 146

RESULT 14
US-08-966-317-3
/ Sequence 3, Application US/09489770
/ Patent No. 6393f01
/ GENERAL INFORMATION:
/ APPLICANT: Hawkins, Phillip R.
/ APPLICANT: Bandman, Olga
/ APPLICANT: Guegler, Karl J.
/ APPLICANT: Shah, Purvi
/ APPLICANT: Corley, Neil C.
/ TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Dr.
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/966,317
/ FILING DATE: Filed Herewith
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
```

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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/489,770
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/966,317
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0403 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-855-0555
/ TELEFAX: 650-845-4166
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 146 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GenBank
/ CLONE: 984837
/ US-09-489-770-3

Query Match 42.8%; Score 350; DB 4; Length 146;
Best Local Similarity 53.1%; Pred. No. 4.9e-30;
Matches 68; Conservative 9; Mismatches 49; Indels 2; Gaps 2;

QY 17 VTGNLVQFGVMIEKMTGKSA-LQYNDYGCYGGSHWPDVDTWCCHAHDCCYGRLEKL 75
DB 19 VQGNIAQFGEMIRLTKGRAELSYAFYGHGGLGGSPKDATDRCCVTHDCCYKSLKS 78

QY 76 GCEPKLEKYLFSVSRGIFC-AGRTTCORLTCECDKRAALCFRRNLGTYNRYAHYPNKL 134
DB 79 GCGTKLLKYKSHQGQITCSANQNSCQRLCQCDKAAAECPARNKKTYSLKYYQFYPNMF 138

QY 135 CTGPTPPC 142
DB 139 CKGKKPKC 146

RESULT 15
US-08-966-317-4
/ Sequence 4, Application US/08966317
/ Patent No. 6103469
/ GENERAL INFORMATION:
/ APPLICANT: Hawkins, Phillip R.
/ APPLICANT: Bandman, Olga
/ APPLICANT: Guegler, Karl J.
/ APPLICANT: Shah, Purvi
/ APPLICANT: Corley, Neil C.
/ TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Dr.
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/966,317
/ FILING DATE: Filed Herewith
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 3, 2004, 05:17:51 ; Search time 50.3698 Seconds
(without alignments)
877.555 Million cell updates/sec

Title: US-10-088-092A-30

Perfect score: 817

Sequence: 1 MKSPHLVFLCLLVALVTGN.....YNRKYAHYPNKLCTGTPPC 142

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 1276540

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	370	45.3	164	9	US-09-925-300-1010
3	368.5	45.1	144	10	US-09-975-456B-6
4	368.5	45.1	144	14	US-10-205-823-325
5	368.5	45.1	144	15	US-10-116-275-269
6	360.5	44.1	124	14	US-10-255-576-2
7	350	42.8	146	9	US-09-993-999-8
8	350	42.8	146	13	US-10-124-591-3
9	349.5	42.8	138	12	US-09-917-805-7
10	349.5	42.8	146	13	US-10-124-591-4
11	345.5	42.3	138	12	US-09-917-805-6
12	325.5	39.8	138	12	US-09-917-805-2
13	317.5	38.9	138	10	US-09-975-456B-9
14	310.5	38.0	145	9	US-09-969-384-17
15	310.5	38.0	145	10	US-09-975-456B-7

16	309	37.8	168	10	US-09-975-456B-2	Sequence 2, Appli
17	309	37.8	168	15	US-10-104-047-3735	Sequence 3735, Ap
18	309	37.8	211	14	US-10-345-680-23	Sequence 23, Appl
19	309	37.8	211	15	US-10-295-027-135	Sequence 195, App
20	309	37.8	211	16	US-10-275-998-2	Sequence 2, Appli
21	309	37.8	211	16	US-10-188-832-80	Sequence 80, Appl
22	308.5	37.8	145	9	US-09-835-996A-6	Sequence 6, Appli
23	308.5	37.8	150	12	US-10-296-115-1342	Sequence 1342, Ap
24	306.5	37.5	137	9	US-09-993-999-9	Sequence 9, Appli
25	299.5	36.7	118	9	US-09-987-655-5	Sequence 5, Appli
26	299.5	36.7	118	9	US-09-987-675-5	Sequence 5, Appli
27	287.5	35.2	155	10	US-09-975-456B-10	Sequence 10, Appl
28	287.5	35.2	165	13	US-10-124-591-1	Sequence 1, Appli
29	283.5	34.7	145	12	US-09-917-805-9	Sequence 9, Appli
30	281	34.4	145	12	US-09-917-805-4	Sequence 4, Appli
31	260	31.8	145	12	US-09-917-805-5	Sequence 5, Appli
32	231.5	28.3	145	12	US-09-917-805-8	Sequence 8, Appli
33	229.5	28.1	146	12	US-09-917-805-1	Sequence 1, Appli
34	227.5	27.8	148	10	US-09-975-456B-5	Sequence 5, Appli
35	227.5	27.8	148	12	US-09-917-805-3	Sequence 3, Appli
36	227.5	27.8	156	9	US-09-925-297-511	Sequence 511, App
37	225	27.5	146	9	US-09-993-999-7	Sequence 7, Appli
38	210	25.7	151	12	US-10-398-663-7	Sequence 7, Appli
39	203.5	24.9	152	14	US-10-230-058A-15	Sequence 15, Appl
40	193.5	23.7	133	15	US-10-371-725-7	Sequence 7, Appli
41	193	23.6	116	10	US-09-946-374-378	Sequence 378, App
42	193	23.6	116	12	US-10-147-493-534	Sequence 534, App
43	193	23.6	116	12	US-10-145-127-534	Sequence 534, App
44	193	23.6	116	12	US-10-160-503-534	Sequence 534, App
45	193	23.6	116	12	US-10-143-118-534	Sequence 534, App

ALIGNMENTS

RESULT 1

US-09-975-456B-8
; Sequence 8, Application US/09975456B
; Publication No. US20030073087A1
; GENERAL INFORMATION:
; APPLICANT: LAZDUNSKI, MICHEL
; APPLICANT: LAMBEAU, GERARD
; APPLICANT: VALENTIN, EMMANUEL
; TITLE OF INVENTION: NOVEL MANVALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2
; FILE REFERENCE: 1478-R-00
; CURRENT APPLICATION NUMBER: US/09/975,456B
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/239,491
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 2.1
; SEQ ID NO 8
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-975-456B-8

Query Match	100.08;	Score	817;	DB	10;	Length	154;
Best-Local Similarity	100.08;	Pred. No.	8.9e-82;	Mismatches	0;	Indels	0;
Matches	142;	Conservative	0;	Indels	0;	Gaps	0;
Qy	1	MKSPHLVFLCLLVALVTGNLVQFGVMIKMTKGSALQYNDYGYCGIGGSHWPDQTDW	60				
Db	13	MKSPHLVFLCLLVALVTGNLVQFGVMIKMTKGSALQYNDYGYCGIGGSHWPDQTDW	72				
Qy	61	CCHAHDCCYGRLKGLCEPKLEKYLFSVSRGIFCAGRTTCQRLTCECDKKAALCFRRNL	120				
Db	73	CCHAHDCCYGRLKGLCEPKLEKYLFSVSRGIFCAGRTTCQRLTCECDKKAALCFRRNL	132				
Qy	121	GTYNRKAYAFYFNKLCGTGTPPC	142				
Db	133	GTYNRKAYAFYFNKLCGTGTPPC	154				

APPLICANT: Lambkin, Imelda
APPLICANT: Higgins, Lisa
TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
FILE REFERENCE: E1067/20087
CURRENT APPLICATION NUMBER: US/10/116,275
CURRENT FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 349
SOFTWARE: PatentIn version 3.1
SEQ ID NO 269
LENGTH: 144
TYPE: PRT
ORGANISM: Homo sapiens
US-10-116-275-269

Query Match 45.1%; Score 368.5; DB 15; Length 144;
Best Local Similarity 52.1%; Pred. No. 1.8e-32;
Matches 73; Conservative 12; Mismatches 46; Indels 9; Gaps 2;
QY 12 LLVALVT-----GNLVFGVMIEKMTGK-SALQNDYGCYGGSHWPVDQTDWCC 62
DB 5 LLLAVIMIFGLQAHGNLVNFRHMIKLTGKEAALSYGFYCHGCGVGRGSPKDATDRCC 64
QY 63 HAHDCYGRLEKLCCEPKLEKLFVSERGIFFCAGRTTCQRLTCECDKRAALCFRNLTGT 122
DB 65 VTHDCCYRLEKRCGCTGKFLSYKFSNSGSRITCAKQDSRCSQICECDKAAATCFARNKT 124
QY 123 YNRKYAHYPNNKLTGPTTPC 142
DB 125 YNKKYQYYSNKHCRGSTPRC 144

RESULT 6
US-10-255-576-2
Sequence 2, Application US/10255576
Publication No. US20030161822A1
GENERAL INFORMATION:
APPLICANT: Weiss, Jerrold
APPLICANT: Eisbach, Peter
APPLICANT: Liang, Ning-Sheng
TITLE OF INVENTION: ANTIBACTERIAL GROUP IIA PHOSPHOLIPASE A2 AND METHODS OF USE THERE
FILE REFERENCE: 5986/1E917U51
CURRENT APPLICATION NUMBER: US/10/255,576
CURRENT FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: US/09/740,569
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US 60/172,467
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 124
TYPE: PRT
ORGANISM: Homo sapiens
US-10-255-576-2

Query Match 44.1%; Score 360.5; DB 14; Length 124;
Best Local Similarity 54.8%; Pred. No. 1.2e-31;
Matches 68; Conservative 11; Mismatches 44; Indels 1; Gaps 1;
QY 20 NLVQFGVMIEKMTGK-SALQNDYGCYGGSHWPVDQTDWCCCHADCCYGRLEKLCGE 78
DB 1 NLNVFRLILKLTGKEAALSYGFYCHGCGVGRGSPKDATDRCCVTHDCCYKRLKRGCG 60
QY 79 PKLEKLFVSERGIFFCAGRTTCQRLTCECDKRAALCFRNLTGTNRKYAHYPNNKLTGP 138
DB 61 TKFLSYKFSNSKSRITCAKQDSRCSQICECDKAAATCFARNKTYNKKYQYYSNKHCRGS 120
QY 139 TTPC 142
DB 121 TTPC 124

RESULT 7
US-09-993-999-8
Sequence 8, Application US/09993999
Patent No. US20020110891A1
GENERAL INFORMATION:
APPLICANT: Ho, I-Cheng
APPLICANT: Arm, Jonathan P.
APPLICANT: Austen, K. Frank
APPLICANT: Glimcher, Laurie H.
TITLE OF INVENTION: Phospholipase A2 Group Preferentially
TITLE OF INVENTION: Expressed in Th2 Cells
FILE REFERENCE: HUI-046
CURRENT APPLICATION NUMBER: US/09/993,999
CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: 60/246,316
PRIOR FILING DATE: 2000-11-06
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 146
TYPE: PRT
ORGANISM: Mus musculus
US-09-993-999-8

Query Match 42.8%; Score 350; DB 9; Length 146;
Best Local Similarity 53.1%; Pred. No. 2e-30;
Matches 68; Conservative 9; Mismatches 49; Indels 2; Gaps 2;
QY 17 VTGNLVQFGVMIEKMTGKSA-LQYNDYGCYGGSHWPVDQTDWCCCHADCCYGRLEK 75
DB 19 VQGNIAQFGEMIRLKTGRAELSYAFYCHGCGVGRGSPKDATDRCCVTHDCCYKSLKS 78
QY 76 GCEPKLEKLFVSERGIFFCAGRTTCQRLTCECDKRAALCFRNLTGTNRKYAHYPNNK 134
DB 79 GCGTKLLKYKSHQGGQITCSANQNSCQKRLCQCDKAAAEFCFARNKTYSLKYQYFNNF 138
QY 135 CTGPTTPC 142
DB 139 CKGKPKC 146

RESULT 8
US-10-124-591-3
Sequence 3, Application US/10124591
Publication No. US20020177208A1
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
APPLICANT: Bandman, Olga
APPLICANT: Guegler, Karl J.
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,591
FILING DATE: 16-Apr-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/489,770
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/966,317
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0403 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 984837

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-124-591-3

Query Match 42.8%; Score 350; DB 13; Length 146;

Best Local Similarity 53.1%; Pred. No. 2e-30;

Matches 68; Conservative 9; Mismatches 49; Indels 2; Gaps 2;

QY 17 VTGNLVQGVMIKMTGKSA-LQYNDYGCYCGIGGSHWPVDQTDWCCHADCCYGRLEKL 75

DB 19 VQNLAFQGVMIKMTGKSA-LQYNDYGCYCGIGGSHWPVDQTDWCCHADCCYGRLEKL 78

QY 76 GCEPKLEKLFVSVERGIFC-AGRTTCQRLTCECDKRAALCFRRNLGTYNRKYAHYPNKL 134

DB 79 CGGTKLLKYSHQGQITCSANQNSQKRLQCDKAAECFARNKXTYSLKTYQFVPMF 138

QY 135 CTGPTPPC 142

DB 139 CKGKKPKC 146

RESULT 9

US-09-917-805-7

Sequence 7; Application US/09917805

Publication No. US20040073973A1

GENERAL INFORMATION:

APPLICANT: STYME, Sten

APPLICANT: STAHL, Ulf

APPLICANT: EK, Bo

APPLICANT: SJODAHL, Staffan

TITLE OF INVENTION: PLANT ENZYME AND USE THEREOF

FILE REFERENCE: STYME-1

CURRENT APPLICATION NUMBER: US/09/917,805

CURRENT FILING DATE: 2001-07-31

PRIOR APPLICATION NUMBER: 09/155,124

PRIOR FILING DATE: 1999-03-02

PRIOR APPLICATION NUMBER: PCT/SE97/00554

PRIOR FILING DATE: 1997-03-27

PRIOR APPLICATION NUMBER: 9601237.2

PRIOR FILING DATE: 1996-03-29

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 7

LENGTH: 138

TYPE: PRT

ORGANISM: Bothrops jararacussu

US-09-917-805-7

Query Match

Best Local Similarity 42.8%; Score 349.5; DB 12; Length 138;

Matches 66; Conservative 15; Mismatches 53; Indels 3; Gaps 2;

QY 7 LVFLCLLVALVTGNLVQGVMIKMTGKSA-LQYNDYGCYCGIGGSHWPVDQTDWCCHAH 65

DB 4 LWIMAVLLVGVGDLWQFGQMLKETGLPFYTYTCYCGWGGQGPQKDATDRCCFVH 63

QY 66 DCCYGRLEKLEKLFVSVERGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNR 125

DB 64 DCCYVKL--TNCKPKTDYRSYRENGVTCGEGTFCCKQICECDKAAVCFRRNLRTYK 121

QY 126 KYAHYPNKLCTGPTPPC 142

DB 122 RYMAVPDVLCKKPAKC 138

RESULT 10

US-10-124-591-4

Sequence 4; Application US/10124591

Publication No. US20020177208A1

GENERAL INFORMATION:

APPLICANT: Hawkins, Phillip R.

Bandman, Olga

Guegler, Karl J.

Shah, Purvi

Corley, Neil C.

TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Dr.

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/124,591

FILING DATE: 16-Apr-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/489,770

FILING DATE: <Unknown>

APPLICATION NUMBER: 08/966,317

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0403 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 146 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GenBank

CLONE: 204319

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-124-591-4

Query Match 42.8%; Score 349.5; DB 13; Length 146;

Best Local Similarity 47.2%; Pred. No. 2.3e-30;

Matches 68; Conservative 18; Mismatches 51; Indels 7; Gaps 3;

QY 6 VLAVFLCLLVAL-----VTGNLVQGVMIKMTGKSA-LQYNDYGCYCGIGGSHWPVDQTD 59

DB 3 VILLAVVIMAFGSTQVQGSLLFQGMILFKTKRADVSYGYGCHGCGVGGSGPKDATD 62

QY 60 WCHAHADCCYGRLEKLEKLFVSVERGIFC-GRITTCQRLTCECDKRAALCFRR 118

DB 63 WCVTHDCCYNLEKRGCGTKLTLYKFSYRGQISCTNQDSCKRLQCCDCAAECEAR 122

QY 119 NLGTYNRYAHYPNKLCTGPTPPC 142

DB 123 NKKSVSLKYQFYLNKFCGKGTPTSC 146

```
RESULT 11
US-09-917-805-6
; Sequence 6, Application US/09917805
; Publication No. US20040073973A1
; GENERAL INFORMATION:
; APPLICANT: STYNE, Sten
; APPLICANT: STAHL, Ulf
; APPLICANT: EK, Bo
; APPLICANT: SJODAHL, Staffan
; TITLE OF INVENTION: PLANT ENZYME AND USE THEREOF
; FILE REFERENCE: STYNE=1
; CURRENT APPLICATION NUMBER: US/09/917,805
; CURRENT FILING DATE: 2001-07-31
; PRIOR FILING DATE: 1999-03-27
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: PCT/SE97/00554
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: 9601237.2
; PRIOR FILING DATE: 1996-03-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Vipera ammodytes
US-09-917-805-6

Query Match      42.3%; Score 345.5; DB 12; Length 138;
Best Local Similarity 46.7%; Pred. No. 5.9e-30;
Matches 64; Conservative 21; Mismatches 47; Indels 5; Gaps 3;

QY 7 LVFLCLLVALVTGNLVQFGVMIEKMTGKSA-LQNDYGCYCGIGGSHWPVDQTDWCCHAH 65
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6 IVAVCLIG--VEGSLLEFGNMILGETGKNPLTSFYGCYCGVGKGTPKDATDRCCFVH 63
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 66 DCCYGRLEKLGCEPKLEKYLFSVSERGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNR 125
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 64 DCCYGNLP--DCSPKTDRIYHRENGALVCGKGTSCENRICEDRAAALCFRRNLGTYN 121
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 126 KYAHYPNKLCTGTPPC 142
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 122 IYRNPDFLCKESEKC 138
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
US-09-917-805-2
; Sequence 2, Application US/09917805
; Publication No. US20040073973A1
; GENERAL INFORMATION:
; APPLICANT: STYNE, Sten
; APPLICANT: STAHL, Ulf
; APPLICANT: EK, Bo
; APPLICANT: SJODAHL, Staffan
; TITLE OF INVENTION: PLANT ENZYME AND USE THEREOF
; FILE REFERENCE: STYNE=1
; CURRENT APPLICATION NUMBER: US/09/917,805
; CURRENT FILING DATE: 2001-07-31
; PRIOR FILING DATE: 1999-03-02
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: PCT/SE97/00554
; PRIOR FILING DATE: 1996-03-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Trimeresurus flavoviridis
US-09-917-805-2
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```
Query Match      39.8%; Score 325.5; DB 12; Length 138;
Best Local Similarity 48.6%; Pred. No. 9.4e-28;
Matches 67; Conservative 15; Mismatches 51; Indels 5; Gaps 4;

QY 7 LVFLCLLVALVTGNLVQFGVMIEKMTGKSA-LQNDYGCYCGIGGSHWPVDQTDWCCHAH 65
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 4 LWIMAVLLVGVGGGLWQFENMIKVKKSGILSYSGYCGYCGWGGRGPKDADRCCFVH 63
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 66 DCCYGRLEKLGCEPKLEKYLFSVSERGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNR 125
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 64 DCCYGV--TGCNPKLGKTYTSWNGDIVCGDGPCKEV-CECDRAAALCFRRNLDTYDR 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 126 KYAHYPNKLCTGTPPC 142
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 NKWRYPASNCQEDSEPC 138
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
US-09-975-456B-9
; Sequence 9, Application US/09975456B
; Publication No. US20030073087A1
; GENERAL INFORMATION:
; APPLICANT: LAZDUNSKI, MICHEL
; APPLICANT: LAMBEAU, GERAED
; APPLICANT: VALENTIN, EMMANUEL
; TITLE OF INVENTION: NOVEL MAMMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2
; FILE REFERENCE: 1478-R-00
; CURRENT APPLICATION NUMBER: US/09/975,456B
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/239,491
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 2.1
; SEQ ID NO 9
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-975-456B-9

Query Match      38.9%; Score 317.5; DB 10; Length 138;
Best Local Similarity 45.7%; Pred. No. 7.1e-27;
Matches 59; Conservative 17; Mismatches 52; Indels 1; Gaps 1;

QY 9 ELCLLVALVTGNLVQFGVMIEKMTGKSA-LQNDYGCYCGIGGSHWPVDQTDWCCHADC 67
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 10 FLACSVPAVQGGLLDLKSMIEKVTGNALTYGFCYCGWGGRGTPDKGTDWCCHADH 69
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 68 CYGRLEKLGCEPKLEKYLFSVSERGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRY 127
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 70 CYGRLEKGCNIRTQSYKYRFAWGVVTCPPGPFCHVNLCACDKRLVYCLKENLRSYNPOY 129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 128 AHYPNKLCT 136
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 130 QYFPNILCS 138
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
US-09-969-384-17
; Sequence 17, Application US/09969384
; Publication No. US20020192749A1
; GENERAL INFORMATION:
; APPLICANT: Moore, et al.
; TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT055PI
; CURRENT APPLICATION NUMBER: US/09/969,384
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/10542
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/236,384
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/194,118
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 27
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-969-384-17

Query Match      38.0%; Score 310.5; DB 9; Length 145;
Best Local Similarity 39.2%; Pred. No. 4.5e-26;
Matches 56; Conservative 23; Mismatches 57; Indels 7; Gaps 3;

Qy 7 LVFLCLLVAL-----VTGNLVQFGVMIEKMTGK-SALQYNDYGCYCGIGGSHWPDQTDW 60
Db 3 LALLCGLVWVAGVPIQGGILNLNKMVKQVTGKMPILSYWPYGCCHGGLGGGQPKDATDW 62

Qy 61 CCHAHDCCYGRLEKLGCEPKLEKYLFSVSRGIFCAGR-TTCORLTCECDKRAALCFRRN 119
Db 63 CCQTHDCCYDHLKTQGGSIYKDYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRN 122

Qy 120 LGTYNRKYAHYPNKLCTGTPPPC 142
Db 123 LDTYQKRLRFYWRPHCRGQTGPGC 145

RESULT 15
US-09-975-456B-7
; Sequence 7, Application US/09975456B
; Publication No. US20030073087A1
; GENERAL INFORMATION:
; APPLICANT: LAMBEAU, MICHEL
; APPLICANT: LAMBEAU, GERARD
; APPLICANT: VALENTIN, EMANUEL
; TITLE OF INVENTION: NOVEL MAMMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2
; FILE REFERENCE: 1478-R-00
; CURRENT APPLICATION NUMBER: US/09/975,456B
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/239,491
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 2.1
; SEQ ID NO 7
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-975-456B-7

Query Match      38.0%; Score 310.5; DB 10; Length 145;
Best Local Similarity 39.2%; Pred. No. 4.5e-26;
Matches 56; Conservative 23; Mismatches 57; Indels 7; Gaps 3;

Qy 7 LVFLCLLVAL-----VTGNLVQFGVMIEKMTGK-SALQYNDYGCYCGIGGSHWPDQTDW 60
Db 3 LALLCGLVWVAGVPIQGGILNLNKMVKQVTGKMPILSYWPYGCCHGGLGGGQPKDATDW 62

Qy 61 CCHAHDCCYGRLEKLGCEPKLEKYLFSVSRGIFCAGR-TTCORLTCECDKRAALCFRRN 119
Db 63 CCQTHDCCYDHLKTQGGSIYKDYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRN 122

Qy 120 LGTYNRKYAHYPNKLCTGTPPPC 142
Db 123 LDTYQKRLRFYWRPHCRGQTGPGC 145

Search completed: July 3, 2004, 05:27:05
Job time : 52.3698 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 3, 2004, 05:12:38 ; Search time 10.1811 Seconds
(without alignments)
726.242 Million cell updates/sec

Title: US-10-088-092A-30

Perfect score: 817

Sequence: 1 MKSPHVLVFLCLLVALVTGN.....YNEKYAHYPNKLCTGTPPC 142

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	817	100.0	142	1	PA2E_HUMAN
2	709	86.8	142	1	PA2E_MOUSE
3	373	45.7	137	1	PA2M_VIPAA
4	372	45.5	121	1	PA21_ERIMA
5	368.5	45.1	144	1	PA2A_HUMAN
6	359.5	44.0	146	1	PA2A_RAT
7	358.5	43.9	120	1	PA2Y_CERCE
8	358.5	43.9	138	1	PA2Q_TRIFL
9	355.5	43.5	138	1	PA2Y_DABRR
10	355	43.5	121	1	PA2B_DABRR
11	354	43.3	137	1	PA2B_VIPAA
12	351.5	43.0	138	1	PA2B_VIPAA
13	351.5	43.0	138	1	PA2M_TRIFL
14	350	42.8	123	1	PA21_AGKPI
15	350	42.8	146	1	PA2A_MOUSE
16	349.5	42.8	138	1	PA21_BOTJR
17	348.5	42.7	138	1	PA26_TRIGA
18	348.5	42.7	138	1	PA2B_VIPAA
19	345.5	42.3	138	1	PA2A_VIPAA
20	345.5	42.3	138	1	PA2C_VIPAA
21	341.5	41.8	138	1	PA2A_TRIFL
22	340.5	41.7	122	1	PA2A_TRIFL
23	340	41.6	121	1	PA2C_BITCA
24	339.5	41.6	122	1	PA2K_TRIFL
25	339.5	41.6	138	1	PA2P_TRIFL
26	338.5	41.4	122	1	PA2B_AGKHP
27	338.5	41.4	122	1	PA2B_TRIFL
28	338.5	41.4	138	1	PA22_TRIMU
29	338.5	41.4	138	1	PA2A_TRIMU
30	336	41.1	145	1	PA2M_CAVPO
31	333.5	40.8	138	1	PA21_TRIGA
32	333.5	40.8	138	1	PA25_ECHOC
33	332.5	40.7	121	1	PA2B_DABRR

RESULT 1
PA2E_HUMAN
ID PA2E_HUMAN STANDARD; PRT; 142 AA.
AC Q9NZK7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Group IIE secretory phospholipase A2 precursor (EC 3.1.1.4)
DE (Phosphatidylcholine 2-acylhydrolase GIIE) (GIIE SPLA2) (SPLA(2)-IIE).
GN PLA2G2E.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX MEDLINE=2014788; PubMed=10681567;
RA Suzuki N., Ishizaki J., Yokota Y., Higashino K., Ono T., Ikeda M.,
RA Fujii N., Kawamoto K., Hanasaki K.;
RT "Structures, enzymatic properties, and expression of novel human and
mouse secretory phospholipase A(2)s";
RL J. Biol. Chem. 275:5785-5793(2000).
CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides. Has a preference for arachidonic-containing phospholipids.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a fatty acid anion.
CC -!- COFACTOR: Binds 1 calcium ion per subunit.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Restricted to the brain, heart, lung, and placenta.
CC -!- SIMILARITY: Belongs to the phospholipase A2 family.

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EMBL; AF189279; AAF36541.1; --
RSP; P14555; IPOD.
DR GO; GO:0004624; F:secretated phospholipase A2 activity; TAS.
DR GO; GO:0005954; P:inflammatory response; TAS.
DR GO; GO:0005644; P:phospholipid metabolism; TAS.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; Phoslip; 1
DR PRINTS; PR00389; PHPLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2c; 1.
DR PROSITE; PS00119; PA2_ASP; FALSE_NEG.
DR PROSITE; PS00118; PA2_HIS; 1.
KW Hydrolase; Lipid degradation; Signal; Calcium.
FT SIGNAL 1 19
FT CHAIN 20 142
FT GROUP IIE SECRETORY PHOSPHOLIPASE A2.

P20249 agkistrodon
P31854 vipera beru
P18998 crocatus sc
P81478 trimeresuru
Q9wvf6 mus musculus
P04417 agkistrodon
Q9pvf2 agkistrodon
Q90z29 echis color
P24294 eristocophi
O42192 agkistrodon
P06859 trimeresuru
P81480 trimeresuru

ALIGNMENTS

34 332.5 40.7 122 1 PA22_AGKHA
35 332.5 40.7 122 1 PA2_VIPBB
36 332.5 40.7 138 1 PA2A_CROSS
37 329.5 40.3 122 1 PA22_TRIGA
38 329 40.3 144 1 PA2D_MOUSE
39 328.5 40.2 122 1 PA21_AGKHA
40 328 40.1 139 1 PA2E_AGKHP
41 326.5 40.0 138 1 PA21_ECHCO
42 325.5 39.8 121 1 PA22_BRIMA
43 325.5 39.8 122 1 PA28_AGKHP
44 325.5 39.8 138 1 PA21_TRIFL
45 324.5 39.7 122 1 PA23_TRIGA

FT ACT SITE 65 BY SIMILARITY.
 FT ACT_SITE 109 BY SIMILARITY.
 FT DISULFID 44 135 BY SIMILARITY.
 FT DISULFID 46 62 BY SIMILARITY.
 FT DISULFID 61 115 BY SIMILARITY.
 FT DISULFID 67 142 BY SIMILARITY.
 FT DISULFID 68 108 BY SIMILARITY.
 FT DISULFID 77 101 BY SIMILARITY.
 FT DISULFID 95 106 BY SIMILARITY.
 FT METAL 45 CALCIUM (VIA CARBONYL OXYGEN)
 FT METAL 47 (BY SIMILARITY).
 FT METAL 47 CALCIUM (VIA CARBONYL OXYGEN)
 FT METAL 49 CALCIUM (VIA CARBONYL OXYGEN)
 FT METAL 49 CALCIUM (VIA CARBONYL OXYGEN)
 FT METAL 66 CALCIUM (BY SIMILARITY).
 FT METAL 66 CALCIUM (BY SIMILARITY).
 SQ SEQUENCE 142 AA; 15989 MW; 3C360EA710E141FB CRC64;
 Query Match 100.0%; Score 817; DB 1; Length 142;
 Best Local Similarity 100.0%; Pred. No. 1e-79;
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKSPHVLVFLCLLVLTGNLVQFGVMTKGSALQYNDYGCYGGGSHWPDQTDW 60
 DB 1 MKSPHVLVFLCLLVLTGNLVQFGVMTKGSALQYNDYGCYGGGSHWPDQTDW 60
 QY 61 CCHADCCYGRLEKLGCEPKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRNL 120
 DB 61 CCHADCCYGRLEKLGCEPKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRNL 120
 QY 121 GTYRKAYHYPNKLCTGTPPC 142
 DB 121 GTYRKAYHYPNKLCTGTPPC 142
 RESULT 2
 ID PA2E_MOUSE STANDARD; PRT; 142 AA.
 AC Q9QUL3;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Group IIE secretory phospholipase A2 precursor (EC 3.1.1.4)
 DE (Phosphatidylcholine 2-acylhydrolase GIIE) (GIIE sPLA2) (sPLA2(2)-IIE).
 GN PLA2G2E.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2002639; PubMed=10531313;
 RA Valentin E., Ghomashchi F., Gelb M.H., Lazdunski M., Lambeau G.;
 RA Suzuki N., Ishizaki J., Yokota Y., Higashino K., Ono T., Ikeda M.,
 RA Fujii N., Kawamoto K., Hanasaki K.;
 RA "Structures, enzymatic properties, and expression of novel human and
 mouse secretory phospholipase A(2)s";
 RL J. Biol. Chem. 275:5785-5793 (2000).
 CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
 acyl groups in 3-sn-phosphoglycerides.
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 acylglycerophosphocholine + a fatty acid anion.
 CC -!- COFACTOR: Binds 1 calcium ion per subunit.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Highly expressed in uterus, and at lower

CC levels in various other tissues.
 CC -!- SIMILARITY: Belongs to the phospholipase A2 family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF166098; AAF04499.1; -;
 CC EMBL; AF122984; AAF22290.1; -;
 CC HSSP; F14555; IPOD.
 CC MGD; MGI:1349660; Pla2g2e.
 CC InterPro; IPR001211; PhospholipaseA2.
 CC Pfam; PF00068; phoslip; 1.
 CC PRINTS; PR00389; PPHLIPASEA2.
 CC ProDom; PD000303; PhospholipaseA2; 1.
 CC SMART; SM00085; PA2c; 1.
 CC PROSITE; PS00119; PA2_ASP; FALSE_NEG.
 CC PROSITE; PS00118; PA2_HIS; 1.
 CC Hydrolase; Lipid degradation; Signal; Calcium.
 KW SIGNAL 1 19
 FT CHAIN 20 142
 FT ACT_SITE 65 65
 FT ACT_SITE 109 109
 FT DISULFID 44 135
 FT DISULFID 46 62
 FT DISULFID 61 115
 FT DISULFID 67 142
 FT DISULFID 68 108
 FT DISULFID 77 101
 FT DISULFID 95 106
 FT METAL 45 45
 FT METAL 47 47
 FT METAL 49 49
 FT METAL 66 66
 FT METAL 66 66
 SQ SEQUENCE 142 AA; 15942 MW; 8B0E3CC710A1F946 CRC64;
 Query Match 86.8%; Score 709; DB 1; Length 142;
 Best Local Similarity 84.5%; Pred. No. 3e-68;
 Matches 120; Conservative 6; Mismatches 16; Indels 0; Gaps 0;
 QY 1 MKSPHVLVFLCLLVLTGNLVQFGVMTKGSALQYNDYGCYGGGSHWPDQTDW 60
 DB 1 MKPPTALACLCLLVPLAGNLVQFGVMTKGSALQYNDYGCYGGGSHWPDQTDW 60
 QY 61 CCHADCCYGRLEKLGCEPKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRNL 120
 DB 61 CCHADCCYGRLEKLGCEPKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRNL 120
 QY 121 GTYRKAYHYPNKLCTGTPPC 142
 DB 121 NTYRKAYHYPNKLCTGTPPC 142
 RESULT 3
 ID PA2N_VIPAA STANDARD; PRT; 137 AA.
 AC P34180; Q91967;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 16-FEB-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Phospholipase A2, neutral precursor (EC 3.1.1.4) (Ammodytin I2)
 DE (Phosphatidylcholine 2-acylhydrolase).
 GN AMI2.
 OS Vipera ammodytes ammodytes (Western sand viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scieroglossa; Serpentes; Colubroidea;

Query Match 45.5%; Score 372; DB 1; Length 121;
 Best Local Similarity 56.5%; Pred. No. 1.5e-32;
 Matches 70; Conservative 8; Mismatches 42; Indels 4; Gaps 3;

QY 20 NLVFGVMIKTKSA-LQVNDVCGVCGGGSHFVDQDWCCHADCCYGRLEKLGCE 78
 DB 1 NLYFGKMFRTGKSAIYSYDGYCGWGKGKPLDADRCCFVHDCYGRVN--GCN 58

QY 79 FKLEKYLFSVSERGIFCAGRTTCORLTCECDKRAALCFRNLGTYNRYKAYHYNKLTGTP 138
 DB 59 PKLSTYSFQNGDIVCGDDNACLRVCECDRVAICFGENLTYDKYDYSSQCT-E 117

QY 139 TPPC 142
 DB 118 TEQC 121

RESULT 5
 FAZA HUMAN STANDARD; PRT; 144 AA.

AC P14555; Q3UCD2;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Phospholipase A2, membrane associated precursor (EC 3.1.1.4)
 DE (Phosphatidylcholine 2-acylhydrolase) (Group IIA phospholipase A2)
 DE (GLIC sPLA2) (Non-pancreatic secretory phospholipase A2) (NPS-PLA2).
 GN PLA2G2A OR PLA2B OR RASFA OR PLA2L.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=Rheumatoid arthritic synovial fluid;
 RX MEDLINE=89174566; PubMed=2925608;
 RA Seilhamer J.J., Pruzanski W., Vadas P., Plant S., Miller J.A.,
 RA Kless J., Johnson L.K.;
 RT "Cloning and recombinant expression of phospholipase A2 present in
 RT rheumatoid arthritic synovial fluid.";
 RL J. Biol. Chem. 264:5335-5338(1989).
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=89174633; PubMed=2925633;
 RA Kramer R.M., Hession C., Johansen B., Hayes G., McGray P., Chow E.P.,
 RA Tizard R., Pepinsky R.B.;
 RT "Structure and properties of a human non-pancreatic phospholipase
 RT A2.";
 RL J. Biol. Chem. 264:5768-5775(1989).
 RN [3]

RP SEQUENCE FROM N.A.
 RX MEDLINE=91050834; PubMed=2239446;
 RA Kramer R.M., Johansen B., Hession C., Pepinsky R.B.;
 RT "Structure and properties of a secreted phospholipase A2 from human
 RT platelets.";
 RL Adv. Exp. Med. Biol. 275:35-53(1990).
 RN [4]

RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Matra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]

RP SEQUENCE OF 21-144.
 RC TISSUE=Spleen;
 RX MEDLINE=89374261; PubMed=2775276;
 RA Kanda A., Ono T., Yoshida N., Tojo H., Okamoto M.;
 RT "The primary structure of a membrane-associated phospholipase A2 from
 RT human spleen.";
 RL Biochem. Biophys. Res. Commun. 163:42-48(1989).
 RN [6]

RP SEQUENCE OF 21-54.
 RC TISSUE=Synovial fluid;
 RX MEDLINE=89197814; PubMed=3240982;
 RA Hara S., Kudo I., Matsuta K., Miyamoto T., Inoue K.;
 RT "Amino acid composition and NH2-terminal amino acid sequence of human
 RT phospholipase A2 purified from rheumatoid synovial fluid.";
 RL J. Biochem. 104:326-328(1988).
 RN [7]

RP SEQUENCE OF 21-33.
 RC TISSUE=Synovial fluid;
 RX MEDLINE=89076274; PubMed=3202859;
 RA Lai C.Y., Wada K.;
 RT "Phospholipase A2 from human synovial fluid: purification and
 RT structural homology to the placental enzyme.";
 RL Biochem. Biophys. Res. Commun. 157:488-493(1988).
 RN [8]

RP SEQUENCE OF 21-75.
 RC TISSUE=ileal mucosa;
 RX MEDLINE=94002200; PubMed=8399335;
 RA Minami T., Tojo H., Shinomura Y., Matsuzawa Y., Okamoto M.;
 RT "Purification and characterization of a phospholipase A2 from human
 RT ileal mucosa.";
 RL Biochim. Biophys. Acta 1170:125-130(1993).
 RN [9]

RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=91287826; PubMed=2062381;
 RA Wery J.-P., Schevitz R.W., Clawson D.K., Bobbitt J.L., Dow E.R.,
 RA Gamboa G., Goodson T. Jr., Hermann R.B., Kramer R.M., McClure D.B.,
 RA Mihelich E.D., Putnam J.E., Sharp J.D., Stark D.H., Teater C.,
 RA Warrick M.W., Jones N.D.;
 RT "Structure of recombinant human rheumatoid arthritic synovial fluid
 RT phospholipase A2 at 2.2-A resolution.";
 RL Nature 352:79-82(1991).
 RN [10]

RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=92054586; PubMed=1948070;
 RA Scott D.L., White S.P., Browning J.L., Rosa J.J., Gelb M.H.,
 RA Sigler P.B.;
 RT "Structures of free and inhibited human secretory phospholipase A2
 RT from inflammatory exudate.";
 RL Science 254:1007-1010(1991).
 RN [11]

RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=95393225; PubMed=7664108;
 RA Schevitz R.W., Bach N.J., Carlson D.G., Chirgadze N.Y., Clawson D.K.,
 RA Dillard R.D., Drabheim S.E., Hartley L.W., Jones N.D., Mihelich E.D.,
 RA Olkowski J.L., Snyder D.W., Dand S.C., Wery J.-P.;
 RT "Structure-based design of the first potent and selective inhibitor
 RT of human non-pancreatic secretory phospholipase A2.";
 RL Nat. Struct. Biol. 2:458-465(1995).
 RN [12]

RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=98207049; PubMed=9538252;
 RA Kitadoko K., Hagishita S., Sato T., Ohtan M., Miki K.;
 RT "Crystal structure of human secretory phospholipase A2-IIIa complex
 RT with the potent indolizine inhibitor 120-1032.";

RX MEDLINE=88186890; PubMed=3356705;
 RA Ono T., Tojo H., Kuramitsu S., Kagamiyama H., Okamoto M.;
 RT "Purification and characterization of a membrane-associated
 phospholipase A2 from rat spleen. Its comparison with a cytosolic
 phospholipase A2 S-1.";
 RL J. Biol. Chem. 263:5732-5738(1988).
 RN [7]
 RP SEQUENCE OF 22-46.
 RC TISSUE=Platelet;
 RX MEDLINE=88007474; PubMed=3654593;
 RA Hayakawa M., Horigome K., Kudo I., Tomita M., Nojima S., Inoue K.;
 RT "Amino acid composition and NH2-terminal amino acid sequence of rat
 platelet secretory phospholipase A2.";
 RL J. Biochem. 101:1311-1314(1987).
 RN [8]
 RP SEQUENCE OF 22-45.
 RC TISSUE=Liver;
 RX MEDLINE=89255484; PubMed=2722857;
 RA Aarsman A.J., de Jong J.G.N., Arnoldussen E., Neys F.W.,
 van Wassenaar P.D., van den Bosch H.;
 RT "Immunocaffinity purification, partial sequence, and subcellular
 localization of rat liver phospholipase A2.";
 RL J. Biol. Chem. 264:10008-10014(1989).
 CC -!- FUNCTION: Thought to participate in the regulation of the
 phospholipid metabolism in biomenbranes including eicosanoid
 biosynthesis. Catalyzes the calcium-dependent hydrolysis of the 2-
 acyl groups in 3-sn-phosphoglycerides.
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 acylglycerophosphocholine + a fatty acid anion.
 CC -!- COFACTOR: Binds 1' calcium ion per subunit (By similarity).
 CC -!- SUBCELLULAR LOCATION: Membrane-associated.
 CC -!- MISCELLANEOUS: Group II phospholipase A2 is found in many cells
 and also extracellularly. The membrane-bound and secreted forms
 are identical and are encoded by a single gene.
 CC -!- SIMILARITY: Belongs to the phospholipase A2 family.
 CC
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 or send an email to license@isb-sib.ch).
 CC

 CC EMBL; D00523; BAA00410.1; -;
 DR EMBL; M37127; AAA41231.1; -;
 DR EMBL; M25148; AAA41920.1; -;
 DR EMBL; X51529; CAA35909.1; -;
 DR PIR; A33394; A33394.
 DR HSP; P14555; 1POD.
 DR InterPro; IPR001211; PhospholipaseA2.
 DR PRINTS; PF00068; phoslip; 1.
 DR PRODOM; PD000303; PhospholipaseA2; 1.
 DR SMART; SM00085; PA2c; 1.
 DR PROSITE; PS00118; PA2_HIS; 1.
 DR PROSITE; PS00119; PA2_ASP; 1.
 KW Hydrolase; Lipid degradation; Membrane; Signal; Calcium.
 FT SIGNAL 1 21
 FT CHAIN 22 146
 FT ACT_SITE 68 68
 FT ACT_SITE 113 113
 FT DISULFID 47 139
 FT DISULFID 49 65
 FT DISULFID 64 119
 FT DISULFID 70 146
 FT DISULFID 71 112
 FT DISULFID 80 105
 FT DISULFID 98 110
 FT METAL 48 48
 FT METAL 50 50
 FT METAL
 FT METAL

FT METAL 52 52 CALCIUM (VIA CARBONYL OXYGEN)
 FT METAL 69 69 (BY SIMILARITY).
 FT VARIANT 135 135 CALCIUM (BY SIMILARITY).
 FT CONFLICT 22 22 P -> L (POLYMORPHISM).
 FT CONFLICT 63 63 S -> D (IN REF. 8).
 FT CONFLICT 69 69 W -> E (IN REF. 5).
 FT CONFLICT 69 69 D -> E (IN REF. 5).
 FT CONFLICT 78 78 R -> S (IN REF. 5).
 FT CONFLICT 85 85 L -> V (IN REF. 3).
 FT CONFLICT 121 121 A -> S (IN REF. 5).
 SQ SEQUENCE 146 AA; 16294 MW; 60DDC9E79BF109F7 CRC64;
 Query Match 44.0%; Score 359.5; DB 1; Length 146;
 Best Local Similarity 47.9%; Pred. No. 4e-31; Indels 7; Gaps 3;
 Matches 69; Conservative 18; Mismatches 50;
 QY 6 VLVLFLCLLVAL-----VTGNLVQFGVMIEKMTGKSA-LQYNDYCYGIGGSHWVPQDT 59
 Db 3 VLLLLAVVIMAFGSIQVQSLLEFGQMLFKTKRADVSYGFYGCYGCYGVGSGPKDATD 62
 QY 60 WCCHAHDCYGRLEKLGCEPKLEKYLFSVSERGIFCA-GRITCORLTCECDKRALCFRR 118
 Db 63 MCCVTHDCYNRLEKRGCGTKFLTYKFSYRGQISCSSTNQDSCKRQLCCCKAAAEAFAR 122
 QY 119 NLGTYNRYAHYPNKLCTGTPPC 142
 Db 123 NKXSLKLYQFYPNKFCKGKTPSC 146
 RESULT 7
 PA2 CERCE STANDARD; PRT; 120 AA.
 ID PA2 CERCE
 AC P21789;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Phospholipase A2 (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase).
 OS Cerastes cerastes (Horned desert viper).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
 CC Viperidae; Viperinae; Cerastes.
 CC NCBI_TaxID=8697;
 RN [1]
 RN SEQUENCE.
 RC STRAIN=Baluchistan; TISSUE=Venom;
 RA MEDLINE=91130587; PubMed=1993470;
 RA Siddiqi A.R., Shafqat J., Zaidi Z.H., Joernvall H.;
 RT "Characterization of phospholipase A2 from the venom of Horned viper
 (Cerastes cerastes).";
 RL FEBS Lett. 278:14-16(1991).
 RN [2]
 RN SEQUENCE OF 1-31.
 RC STRAIN=Tunisia; TISSUE=Venom;
 RX MEDLINE=90385487; PubMed=2402760;
 RA Djebbari F.L., Martin-Eauclaire M.-F.;
 RT "Purification and characterization of a phospholipase A2 from
 Cerastes cerastes (horn viper) snake venom.";
 RL Toxicon 28:637-646(1990).
 CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
 acyl groups in 3-sn-phosphoglycerides.
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 acylglycerophosphocholine + a fatty acid anion.
 CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MISCELLANEOUS: Strains variations are extensive for this enzyme.
 CC -!- SIMILARITY: Belongs to the phospholipase A2 family. Group II
 subfamily.
 CC PIR; A35950; A35950.
 DR PIR; S13019; S13019.
 DR HSP; P81458; LVIP.
 DR InterPro; IPR001211; PhospholipaseA2.
 DR Pfam; PF00068; phoslip; 1.
 DR PRINTS; PR00389; PHPLIPASEA2.

ProDom; PD000303; PhospholipaseA2; 1.
 SMART; SM00085; PA2c; 1.
 PROSITE; PS00119; PA2_ASP; 1.
 PROSITE; PS00118; PA2_HIS; 1.
 KW Hydrolyase; Lipid degradation; Calcium.
 FT ACT_SITE 47 47 BY SIMILARITY.
 FT ACT_SITE 89 89 BY SIMILARITY.
 FT DISULFID 26 115 BY SIMILARITY.
 FT DISULFID 28 44 BY SIMILARITY.
 FT DISULFID 43 95 BY SIMILARITY.
 FT DISULFID 50 88 BY SIMILARITY.
 FT DISULFID 57 81 BY SIMILARITY.
 FT DISULFID 75 86 BY SIMILARITY.
 FT METAL 27 27 CALCIUM (VIA CARBONYL OXYGEN)
 FT METAL 29 29 CALCIUM (VIA CARBONYL OXYGEN)
 FT METAL 31 31 CALCIUM (VIA CARBONYL OXYGEN)
 FT METAL 31 31 CALCIUM (VIA CARBONYL OXYGEN)
 FT METAL 48 48 CALCIUM (BY SIMILARITY).
 FT VARIANT 10 12 FKM -> KHK (IN STRAIN TUNISIA).
 FT VARIANT 17 19 PIF -> ALL (IN STRAIN TUNISIA).
 FT VARIANT 22 23 GD -> SA (IN STRAIN TUNISIA).
 SQ SEQUENCE 120 AA; 13534 MW; B5581FA7001C62C3 CRC64;
 Query Match 43.9%; Score 358.5; DB 1; Length 120;
 Best Local Similarity 54.2%; Pred. No. 4.2e-31;
 Matches 64; Conservative 10; Mismatches 41; Indels 3; Gaps 2;
 QY 20 NLVQGVMIKMTGKSGAL-QYNDYGVCGYGGSHWPDQTDWCHAHDCYGRLEKLGCE 78
 DB 1 NLVQGVMIKMTGKSGAL-QYNDYGVCGYGGSHWPDQTDWCHAHDCYGRLEKLGCE 78
 QY 79 PLEKYLFSVSGRIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRKYAHYPNKLCT 136
 DB 59 PKRSTYSYSPQNGIVGCDQNLCKRAVCECDRAALCFRRNLGTYNRKYAHYPNKLCT 136
 RESULT 8
 ID PAZY_TRIFL STANDARD; PRT; 138 AA.
 AC Q90Y77;
 DT 28-FEB-2003 (Rel. 41; Created)
 DT 28-FEB-2003 (Rel. 41; Last sequence update)
 DT 10-OCT-2003 (Rel. 42; Last annotation update)
 DE Phospholipase A2 isozyme PL-Y precursor (EC 3.1.1.4)
 DE (Phosphatidylcholine 2-acylhydrolase).
 OS Trimeresurus flavoviridis (Habu).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Trimeresurus.
 OX NCBI_TaxID=88087;
 RN [1]
 SEQUENCE FROM N.A.
 RA Chijiwa T., Yamaguchi Y., Ogawa T., Deshimaru M., Nobuhisa I.,
 RA Nakashima K.-I., Oda-Ueda N., Shimohigashi Y., Fukumaki Y.,
 RA Hattori S., Ohno M.;
 RT "Regional evolution of Trimeresurus flavoviridis venom-gland
 phospholipase A2 isozymes.";
 RL Submitted (Sep-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the
 CC 2-acyl groups in 3-sn-phosphoglycerides (By similarity).
 CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a fatty acid anion.
 CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland (Probable).
 CC -1- SIMILARITY: Belongs to the phospholipase A2 family. Group II
 CC subfamily.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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use by non-profit institutions as long as its content is in no way
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

 CC EMBL; AB072173; BAB68546.1; -;
 CC InterPro; IPR001211; PhospholipaseA2.
 CC Pfam; PF00068; phoslip; 1.
 CC PRINTS; PR00389; PHPLIPASEA2.
 CC ProDom; PD000303; PhospholipaseA2; 1.
 CC SMART; SM00085; PA2c; 1.
 CC PROSITE; PS00119; PA2_ASP; 1.
 CC PROSITE; PS00118; PA2_HIS; 1.
 KW Hydrolyase; Lipid degradation; Calcium; Multigene family; Signal.
 FT SIGNAL 1 16 BY SIMILARITY.
 FT CHAIN 17 138 PHOSPHOLIPASE A2 ISOZYME PL-Y.
 FT ACT_SITE 63 63 BY SIMILARITY.
 FT ACT_SITE 105 105 BY SIMILARITY.
 FT DISULFID 42 131 BY SIMILARITY.
 FT DISULFID 44 60 BY SIMILARITY.
 FT DISULFID 59 111 BY SIMILARITY.
 FT DISULFID 65 138 BY SIMILARITY.
 FT DISULFID 66 104 BY SIMILARITY.
 FT DISULFID 73 97 BY SIMILARITY.
 FT DISULFID 91 102 BY SIMILARITY.
 FT METAL 43 43 CALCIUM (VIA CARBONYL OXYGEN)
 FT METAL 45 45 CALCIUM (BY SIMILARITY).
 FT METAL 47 47 CALCIUM (VIA CARBONYL OXYGEN)
 FT METAL 47 47 CALCIUM (VIA CARBONYL OXYGEN)
 FT METAL 64 64 CALCIUM (BY SIMILARITY).
 SQ SEQUENCE 138 AA; 15729 MW; C96B1E878C8A1196 CRC64;
 Query Match 43.9%; Score 358.5; DB 1; Length 138;
 Best Local Similarity 47.4%; Pred. No. 4.8e-31;
 Matches 65; Conservative 20; Mismatches 45; Indels 3; Gaps 2;
 QY 7 LVFLCLVALVTGNLVQGVMIKMTGKSGAL-QYNDYGVCGYGGSHWPDQTDWCHAH 65
 DB 4 LWINAVLLVGVGHHLLQFRMKIKMTGKEPIVSFAFYGVCGYGGSHWPDQTDWCHAH 63
 QY 66 DCCYGRLEKLGCEPKLYLFSVSGRIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNR 125
 DB 64 DCCYGRLEKLGCEPKLYLFSVSGRIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNR 125
 QY 126 KYAHYPNKLCTGPTPPC 142
 DB 122 RYMTFPDIFCTDPTTEK 138
 RESULT 9
 ID PAZY_TRIFL STANDARD; PRT; 138 AA.
 AC Q8UJG0;
 DT 28-FEB-2003 (Rel. 41; Created)
 DT 28-FEB-2003 (Rel. 41; Last sequence update)
 DT 10-OCT-2003 (Rel. 42; Last annotation update)
 DE Phospholipase A2 isozyme cPLA-B (A) precursor (EC 3.1.1.4)
 DE (Phosphatidylcholine 2-acylhydrolase).
 OS Trimeresurus flavoviridis (Habu).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Trimeresurus.
 OX NCBI_TaxID=88087;
 RN [1]
 SEQUENCE FROM N.A.
 RA Chijiwa T., Yamaguchi Y., Ogawa T., Deshimaru M., Nobuhisa I.,
 RA Nakashima K.-I., Oda-Ueda N., Shimohigashi Y., Fukumaki Y.,
 RA Hattori S., Ohno M.;
 RT "Interisland evolution of Trimeresurus flavoviridis venom
 phospholipase A(2) isozymes.";

J. Mol. Evol. 56:286-293(2003).

1- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides.

1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a fatty acid anion.

1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).

1- SUBCELLULAR LOCATION: Secreted (Probable).

1- TISSUE SPECIFICITY: Expressed by the venom gland.

1- SIMILARITY: Belongs to the phospholipase A2 family. Group II subfamily.

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EMBL; AB087496; BAC02719.1; -.

InterPro; IPR001211; PhospholipaseA2.

Pfam; PF00068; Phoslip; 1.

PRINTS; PR00389; PHPLIPASEA2.

ProDom; PD000303; PhospholipaseA2; 1.

SMART; SM00085; PA2c; 1.

PROSITE; PS00119; PA2_ASP; 1.

PROSITE; PS00118; PA2_HIS; 1.

Hydrolase; Lipid degradation; Calcium; Multigene family; Signal.

SIGNAL 1 16

CHAIN 17 138

ACT_SITE 63 63

ACT_SITE 105 105

DISULFID 42 131

DISULFID 44 60

DISULFID 59 111

DISULFID 65 138

DISULFID 66 104

DISULFID 73 97

DISULFID 91 102

METAL 43 43

METAL 45 45

METAL 47 47

METAL 64 64

SEQUENCE 138 AA; 15703 MW; CBDE540581DD2F10 CRC64;

Query Match 43.5%; Score 355.5; DB 1; Length 138;

Best Local Similarity 49.2%; Pred. No. 1e-30;

Matches 65; Conservative 17; Mismatches 47; Indels 3; Gaps 2;

Qy 12 LLVALVTGNVYFGVMIEKMTGKSL-QYNDYGCYCGIGGSHMPVDOTDWCCHADCCYG 70

Db 9 VLLGVGELLQFRMKMTGKPIVSYAFYCYCGKGRGPKDTRCCFVDDCCYG 68

Qy 71 RLEKLGCEPKLEKLYFSVSERGIFCAGRTTCORITCECDKRAALCFRNLTGTYNRKYAHY 130

Db 69 KV--TGCDPKWDYTYSSENGDIVCEGDNPTCKEVCEDKAAAIICFRDLNLTYYKRYMTF 126

Qy 131 PNKLTGTPPC 142

Db 127 PDIFCTDPTK 138

RESULT 10

PA2_DABRR STANDARD; PRT; 121 AA.

AC P81458;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Phospholipase A2 RVV-VD (EC 3.1.1.4) (Phosphatidylcholine 2-

DE acylhydrolase).

OS Daboia russelli russelli (Russell's viper) (Vipera russelli russelli).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Viperidae; Viperinae; Daboia.

OX NCBI_TaxID=31159;

RP [1]

RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).

RX TISSUE=Venom;

RX MEDLINE=98267643; PubMed=9604284;

RA Cartedano B., Westerlund B., Persson B., Saarinen M., Ramaswamy S., Baker D., Eklund H.

RT "The three-dimensional structures of two toxins from snake venom throw light on the anticoagulant and neurotoxic sites of phospholipase A2.";

RL Toxicon 36:75-92(1998).

CC 1- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides. This protein has anticoagulant activity.

CC 1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a fatty acid anion.

CC 1- COFACTOR: Binds 1 calcium ion per subunit.

CC 1- SUBUNIT: Monomer.

CC 1- SUBCELLULAR LOCATION: Secreted.

CC 1- SIMILARITY: Belongs to the phospholipase A2 family. Group II subfamily.

CC PDB; 1VIP; 16-JUN-97.

DR InterPro; IPR001211; PhospholipaseA2.

DR Pfam; PF00068; Phoslip; 1.

DR PRINTS; PR00389; PHPLIPASEA2.

DR ProDom; PD000303; PhospholipaseA2; 1.

DR SMART; SM00085; PA2c; 1.

DR PROSITE; PS00119; PA2_ASP; 1.

DR PROSITE; PS00118; PA2_HIS; 1.

KW Hydrolase; Lipid degradation; Calcium; 3D-structure.

FT ACT_SITE 47 47

FT ACT_SITE 89 89

FT DISULFID 26 115

FT DISULFID 28 44

FT DISULFID 43 95

FT DISULFID 49 121

FT DISULFID 50 88

FT DISULFID 57 81

FT DISULFID 75 86

FT METAL 27 27

FT METAL 29 29

FT METAL 31 31

FT METAL 48 48

FT METAL 2 13

FT HELIX 17 20

FT STRAND 23 24

FT TURN 25 27

FT STRAND 28 29

FT HELIX 39 53

FT TURN 54 54

FT HELIX 55 57

FT TURN 59 61

FT STRAND 66 68

FT STRAND 73 75

FT HELIX 80 98

FT TURN 99 102

FT HELIX 105 107

FT STRAND 108 108

FT TURN 109 109

FT HELIX 112 114

SQ SEQUENCE 121 AA; 13626 MW; 98CBC4A8922A89D1 CRC64;

Query Match 43.5%; Score 355; DB 1; Length 121;

Best Local Similarity 53.2%; Pred. No. 9.9e-31;

Matches 66; Conservative 13; Mismatches 41; Indels 4; Gaps 3;

QY	20	NLVQGVGMIEKMTGSAL-QYNIDYCYCGIGSGSHWFPVDOTDWCHAHDCYGRLEKLGCE	78
Db	1	NLUQFAEMITVMTGKNPULSSYSYDGYCYGCGWGKGKQPQDTRDCFCVHDCCYEKVK--SCK	58
QY	79	PKLEKYLFSVSRGIFCAGRTTCQLRTCECDKRAALCFRRNLGTYNNRYKAYFPNKLCITGP	138
Db	59	PKLSLYSYSFQNGIVCGDNHSCKEAVCECDRVAATCFRONLNTYDKKXHYNPPSQTG-	117
QY	139	TPPC 142	
Db	118	TEQC 121	
RESULT 11			
PA28_VIPPA			
ID	PA28_VIPPA	STANDARD;	PRT; 137 AA.
AC	QYGG7;		
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Phospholipase A2 homolog VPA precursor.		
OS	Vipera palaestinae (Palestine viper) (Pseudocerastes palaestinae).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Lepidosauria; Squamata; Scieroglossa; Serpentes; Colubroidea;		
OC	Viperidae; Viperinae; Vipera.		
OC	NCBI_TaxID=48068;		
RN	[1]		
RN	SEQUENCE FROM N.A.		
RP	TISSUE=Liver;		
RC	MEDLINE=99011427; PubMed=9792822;		
RA	Kordis D., Edolah A., Gubensek F.;		
RT	"Positive darwinian selection in Vipera palaestinae phospholipase A2		
RT	genes is unexpectedly limited to the third exon.";		
RL	Biochem. Biophys. Res. Commun. 251:613-619(1998).		
CC	!- FUNCTION: Is not toxic by itself, but the synergistical mixture of		
CC	V7 and VPA is lethal to mice (By similarity).		
CC	!- SUBUNIT: Does not form a complex (By similarity).		
CC	!- SUBCELLULAR LOCATION: Secreted (By similarity).		
CC	!- TISSUE SPECIFICITY: Expressed by the venom gland (Probable).		
CC	!- SIMILARITY: Belongs to the phospholipase A2 family, Group II		
CC	subfamily.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercia		
CC	entities requires a license agreement (See http://www.isb-sib.ch/announcement		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
CC	EMBL; AF091854; AAC78084.1; -.		
DR	HSSP; P81458; LVIP.		
DR	InterPro; IPR001211; PhospholipaseA2.		
DR	Pfam; PF00668; Phoslip; 1.		
DR	PRINTS; PR00369; PHPLIPAS2A.		
DR	ProDom; PD000303; PhospholipaseA2; 1.		
DR	SMART; SM00085; PA2C; 1.		
DR	PROSITE; PS00119; PA2 ASP; 1.		
DR	PROSITE; PS00118; PA2_HIS; 1.		
KW	Toxin; Signal; Multigene family.		
FT	SIGNAL 1 16	BY SIMILARITY.	
FT	CHAIN 17 137	PHOSPHOLIPASE A2 HOMOLOG VPA.	
FT	ACT_SITE 62 62	BY SIMILARITY.	
FT	ACT_SITE 104 104	BY SIMILARITY.	
FT	DISULFID 41 130	BY SIMILARITY.	
FT	DISULFID 43 59	BY SIMILARITY.	
FT	DISULFID 58 110	BY SIMILARITY.	
FT	DISULFID 64 137	BY SIMILARITY.	
FT	DISULFID 65 103	BY SIMILARITY.	
FT	DISULFID 72 96	BY SIMILARITY.	
FT	DISULFID 90 101	BY SIMILARITY.	
SQ	SEQUENCE 137 AA; 15349 NW; 281ACE6F92AE103D9 CRC64;		

J. Protein Chem. 12:187-193(1993).
[2]
SEQUENCE OF 1-23, AND ACYLATION.
TISSUE=Venom;
MEDLINE=88298768; PubMed=3403524;
RA Cho W., Tomasselli A.G., Heinrichson R.L., Kezdy F.J.;
"The chemical basis for interfacial activation of monomeric
phospholipases A2. Autocatalytic derivatization of the enzyme by acyl
transfer from substrate.";
RT J. Biol. Chem. 263:11237-11241(1988).
[3]
CHARACTERIZATION.
TISSUE=Venom;
MEDLINE=85054816; PubMed=6438084;
RA Maraganore J.M., Merutka G., Cho W., Welches W., Kezdy F.J.,
Heinrichson R.L.;
RA "A new class of phospholipases A2 with lysine in place of aspartate
49. Functional consequences for calcium and substrate binding.";
RT J. Biol. Chem. 259:13839-13843(1984).
[4]
X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
TISSUE=Venom;
MEDLINE=97166209; PubMed=9013608;
RA Han S.X., Yoon E.T., Scott D.L., Sigler P.B., Cho W.;
"Structural aspects of interfacial adsorption. A crystallographic and
site-directed mutagenesis study of the phospholipase A2 from the
venom of Agkistrodon piscivorus piscivorus.";
RT J. Biol. Chem. 272:3573-3582(1997).
[5]
FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
acyl groups in 3-sn-phosphoglycerides.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
acylglycerophosphocholine + a fatty acid anion.
CC -!- COFACTOR: Binds 1 calcium ion per subunit.
CC -!- SUBUNIT: Monomer or homodimer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Acylation causes dimerization.
CC -!- SIMILARITY: Belongs to the phospholipase A2 family. Group II
subfamily.
DR PIR; B53872; B53872.
DR PDB; 1VAP; 07-JUL-97.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PR00389; PHEPLIPASEA2.
DR ProDom; PD003303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2c; 1.
DR PROSITE; PS00119; PA2 ASP; 1.
DR PROSITE; PS00118; PA2 HIS; 1.
KW Hydrolase; lipid degradation; Calcium; Lipoprotein; Palmitate;
3D-structure.
KW ACT_SITE 47 47 BY SIMILARITY.
FT ACT_SITE 89 89 BY SIMILARITY.
FT DISULFID 26 116
FT DISULFID 28 44
FT DISULFID 43 95
FT DISULFID 49 123
FT DISULFID 50 88
FT DISULFID 57 81
FT DISULFID 75 86
FT METAL 27 27 CALCIUM (VIA CARBONYL OXYGEN).
FT METAL 29 29 CALCIUM (VIA CARBONYL OXYGEN).
FT METAL 31 31 CALCIUM (VIA CARBONYL OXYGEN).
FT METAL 48 48 CALCIUM.
FT LIPID 7 7 N(6)-palmitoyl lysine.
FT LIPID 10 10 N(6)-palmitoyl lysine.
FT HELIX 2 13
FT HELIX 17 20
FT STRAND 23 24
FT TURN 25 27
FT STRAND 28 29
FT HELIX 39 52
FT TURN 53 53
FT TURN 59 61
FT STRAND 66 69

FT TURN 70 71
FT STRAND 72 75
FT HELIX 80 98
FT TURN 99 99
FT HELIX 100 102
FT HELIX 105 108
FT STRAND 109 109
FT TURN 110 110
FT HELIX 113 116
SQ SEQUENCE 123 AA; 13989 MW; C39986552D990D72 CRC64;
Query Match 42.8%; Score 350; DB 1; Length 123;
Best Local Similarity 52.0%; Pred. No. 3.4e-30;
Matches 65; Conservative 14; Mismatches 42; Indels 4; Gaps 3;
QY 20 NLVQGVWLEKMTGKSA-LQYNDYGCYCGIGSHWPDQTDWCCHADCCYGRLEKGC 78
Db 1 NUFQEKLIKMTGKSGMLWYSAYCYCGWGQPKDQATRCDFVHCCYGVK--TGCN 58
QY 79 PKLEKLYFSVSRGIFCAGRTTCQRLTCECDKRAALCFERNLGTYNRK-YAHYFNKLC 137
Db 59 PMWDIVTVSDNGNIVCGTNPCKKQICECDRAAICFRDNLKTYDSKTYWYPKKNCKE 118
QY 138 PTPPC 142
Db 119 ESEPC 123
RESULT 15
PA2A_MOUSE STANDARD; PRT; 146 AA.
ID PA2A_MOUSE
AC P31482; Q60871;
DT 01-JUL-1993 (Rel. 26, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Phospholipase A2, membrane associated precursor (EC 3.1.1.4)
DE (Phosphatidylcholine 2-acylhydrolase) (Group IIA phospholipase A2)
DE (GIIC sPA2) (Enhancing factor) (EF).
DE GN PLA2G2A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/c;
RA Mulherkar R.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A., AND POLYMORPHISM.
RC STRAIN=BALE/c, and CD-1; TISSUE=Intestine;
RX MEDLINE=95403435; PubMed=7673223;
RA Kennedy B.P., Payette P., Mudgett J., Vadas P., Pruzanski W.,
Yuan M., Tang C., Rancourt D.E., Cromlish W.;
RT "A natural disruption of the secretory group II phospholipase A2 gene
in inbred mouse strains";
RL J. Biol. Chem. 270:22378-22385(1995).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H;
RX MEDLINE=95300227; PubMed=7781071;
RA MacPhee M., Chepenik K.P., Liddell R.A., Nelson K.K., Siracusa L.D.,
Buchberg A.M.;
RT "The secretory phospholipase A2 gene is a candidate for the Mom1
locus, a major modifier of ApCmin-induced intestinal neoplasia";
RL Cell 81:957-966(1995).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abranson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krywinski M.I., Skalska U., Smilus D.E.,
RA Schenck A., Schein J.E., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [5]
RP SEQUENCE OF 22-146 FROM N.A.
RC STRAIN=BALB/c; TISSUE=Small intestine;
RX MEDLINE=94029955; PubMed=8267767;
RA Mulherkar R., Rao R.S., Wagle A.S., Patki V., Deo M.G.;
RT "Enhancing factor, a Paneth cell specific protein from mouse small
intestines: predicted amino acid sequence from RT-PCR amplified cDNA
and its expression.";
RT Biochem. Biophys. Res. Commun. 195:1254-1263 (1993).
RL [6]
RN ERRATUM.
RP MEDLINE=94071967; PubMed=8250944;
RA Mulherkar R., Rao R.S., Wagle A.S., Patki V., Deo M.G.;
RL Biochem. Biophys. Res. Commun. 197:351-352 (1993).
RN [7]
RP PRELIMINARY SEQUENCE OF 22-41.
RC TISSUE=Small intestine;
RX MEDLINE=93146172; PubMed=8425615;
RA Mulherkar R., Rao R.S., Rao L., Patki V., Chauhan V.S., Deo M.G.;
RT "Enhancing factor protein from mouse small intestines belongs to the
phospholipase A2 family.";
RL FEBS Lett 317:263-266 (1993).
CC -!- FUNCTION: May play a role in cell proliferation, by increasing the
binding of EGF to the cells and thereby modulating its action. In
doing so, this isozyme binds to a membrane-associated receptor
distinct from the EGF receptor and which could be a heparan-
sulfate proteoglycan located on the cell membrane.
CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
acyl groups in 3-sn-phosphoglycerides.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
acylglycerophosphocholine + a fatty acid anion.
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Membrane-associated.
CC -!- TISSUE SPECIFICITY: Mainly in the Paneth cells adjacent to the
stem population in the small intestines. Also expressed in
regenerating liver and hyperplastic esophageal epithelium.
CC -!- POLYMORPHISM: In strains 129/Sv, B10.RIII and C57BL/6, a
polymorphism causes a frameshift and premature truncation of the
protein, rendering it inactive. Strains BALB/c, C3H/He, DBA/1,
DBA/2, MEL and NZB/B1N contain the normal protein while strain CD-
1 is heterozygous for the mutation.
CC -!- SIMILARITY: Belongs to the phospholipase A2 family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).

CC EMBL; X74266; CAA52325.1; -;
CC EMBL; U23358; AAC52252.1; -;
CC EMBL; U28244; AAB06315.1; ALT_INIT.
CC EMBL; BC045156; AAH45156.1; -;
CC PIR; I48342; I48342.

DR PIR; S29495; S29495.
DR HSP; P14555; IPOD.
DR MGD; MGI:104642; P1a2g2a.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PR00389; PHPLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SMC0085; PA2C; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
DR PROSITE; PS00119; PA2_ASP; 1.
KW Hydrolase; Lipid degradation; Calcium; Growth regulation; Signal;
KW Membrane; Polymorphism.
FT SIGNAL 1 21 PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED.
FT CHAIN 22 146 BY SIMILARITY.
FT ACT_SITE 68 68 BY SIMILARITY.
FT ACT_SITE 113 113 BY SIMILARITY.
FT DISULFID 47 139 BY SIMILARITY.
FT DISULFID 49 65 BY SIMILARITY.
FT DISULFID 64 119 BY SIMILARITY.
FT DISULFID 70 146 BY SIMILARITY.
FT DISULFID 71 112 BY SIMILARITY.
FT DISULFID 80 105 BY SIMILARITY.
FT DISULFID 98 110 BY SIMILARITY.
FT METAL 48 48 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 50 50 (BY SIMILARITY).
FT METAL 52 52 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 52 52 (BY SIMILARITY).
FT METAL 69 69 CALCIUM (VIA CARBONYL OXYGEN)
FT CONFLICT 19 19 CALCIUM (BY SIMILARITY).
FT CONFLICT 86 86 V -> D (IN REF. 1).
FT CONFLICT 86 86 K -> T (IN REF. 1).
SQ SEQUENCE 146 AA; 16145 MW; AB904F6B3B1BA5C7 CRC64;
Query Match 42.8%; Score 350; DB 1; Length 146;
Best Local Similarity 53.1%; Pred. No. 4e-30;
Matches 68; Conservative 9; Mismatches 49; Indels 2; Gaps 2;
QY 17 VTGNLVQFGWIEKMTGKSA-LQYNDYCYGICGISHWVPVDQDWCCCHADCCYGRLEKL 75
Db 19 YQGNIAQFGEMIRLTKTKRAELSYAFYCHGLGKSGPKDATDRCCVTHDCCYKSLEKS 78
QY 76 GCEPKLEKYLFSVSRGIFC-AGRTTCQRLTCBCDKRAALCFRRNLGTYNRKYAHYPNKL 134
Db 79 GCGTKLLKYKSHQGGQITCSANQNSCQKLCQCDKAAAECAFARKKTKYSLKYQFYPNMF 138
QY 135 CTGPTPPC 142
Db 139 CKGKPKC 146
Search completed: July 3, 2004, 05:16:39
Job time : 10.1811 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 3, 2004, 05:13:08 ; Search time 30.0075 Seconds
(without alignments)
1493.077 Million cell updates/sec

Title: US-10-088-092A-30
Perfect score: 817
Sequence: 1 MKSPHVLVFLCLLVALVTGN.....YNRKYAHYPNKLCTGTPPC 142

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	361.5	44.2	146	11	Q91V34
2	342.5	41.9	138	13	Q7T1D5
3	339.5	41.6	138	13	Q805A3
4	337.5	41.3	138	13	Q8AXY1
5	337.5	41.3	138	13	Q805A2
6	330.5	40.5	138	13	Q7ZTA8
7	329.5	40.3	138	13	Q7ZTA6
8	328.5	40.2	138	13	Q7T1D1
9	327.5	40.1	138	13	Q7T1D4
10	327.5	40.1	138	13	Q7T1D3
11	327.5	40.1	138	13	Q7T1D2
12	322.5	39.5	138	13	Q800C1
13	321.5	39.4	138	13	Q800C2
14	321.5	39.4	138	13	Q7ZTA7
15	317.5	38.9	138	13	Q800C4
16	317.5	38.9	187	4	Q8N435

ALIGNMENTS

RESULT 1

Q91V34 ID Q91V34 PRELIMINARY; PRT; 146 AA.

AC Q91V34; Q91V34; (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 25, Last annotation update)
DE Platelet phospholipase A2 precursor (Fragment).

OS Rattus norvegicus (Rat)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Wistar; TISSUE=Blood;

RA Liu T.T., Liang N.S., Meng Z.Q., Xie Y.A., Kuang Z.P., Li Y.;

RT "Cloning, and sequence determination of rat platelet phospholipase A2

RT from whole blood.";

RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF365363; AAKS2061.1; "

DR GO; GO:0005509; F:calcium ion binding; IEA.

DR GO; GO:0004623; P:phospholipase A2 activity; IEA.

DR GO; GO:0016042; P:lipid catabolism; IEA.

DR InterPro; IPR001211; PhospholipaseA2.

DR Pfam; PF00068; Phoslip; 1.

DR PRINTS; PR00389; PHPLIPASEA2.

DR Prodbm; PD000303; PhospholipaseA2; 1.

DR SMART; SM00085; PA2C; 1.

DR PROSITE; PS00119; PA2 ASP; 1.

DR PROSITE; PS00118; PA2_HIS; 1.

Signal.

FT SIGNAL 1 21 POTENTIAL.

FT CHAIN 22 >146 PLATELET PHOSPHOLIPASE A2.

FT NON TER 146 146

SQ SEQUENCE 146 AA; 16306 MW; 60C1C9EC85DCBD67 CRC64;

Query Match 44.2%; Score 361.5; DB 11; Length 146;

Best Local Similarity 47.9%; Pred. No. 2.4e-33;

Matches 69; Conservative 18; Mismatches 50; Indels 7; Gaps 3;

Q7T2R1 vipera russ
Q800C3 crotalus vi
Q7C3T5 vipera russ
Q7Z2Q1 vipera russ
Q8N217 homo sapien
Q804D7 bothrops ja
Q8B193 mus musculu
Q7T3S7 echis carin
Q8CE14 mus musculu
Q8K0Y1 mus musculu
Q7C1C6 vipera aspi
Q9X6F8 mesocricetu
Q8C5Y6 mus musculu
Q7ZW60 rana catesb
Q8AXW1 bungarus mu
Q8AXW2 bungarus mu
Q7T1R1 bungarus fl
Q8AXW7 micrurus co
Q8AY48 bungarus ca
Q8AXW0 bungarus mu
Q9DEB0 pagrus majo
Q7T2Q4 bungarus fl
Q8WS88 adamsia car
Q7C2Q5 bungarus fl
Q802I1 bungarus ca
Q9YH62 dicentrarch
Q9U8P8 asterina pe
O57313 pagrus majo

17 314.5 38.5 138 13 Q7T2R1
18 313.5 38.4 138 13 Q800C3
19 311.5 38.1 130 13 Q7C3T5
20 311.5 38.1 138 13 Q7Z2Q1
21 309 37.8 168 4 Q8N217
22 306 37.5 137 13 Q804D7
23 305.5 37.4 202 11 Q8B193
24 303 37.1 136 13 Q7T3S7
25 303 37.1 210 11 Q8CE14
26 297.5 36.4 150 11 Q8K0Y1
27 295.5 36.2 138 13 Q7C1C6
28 286.5 35.1 154 11 Q9X6F8
29 280.5 34.3 141 11 Q8C5Y6
30 273.5 33.5 147 13 Q7ZW60
31 267 32.7 147 13 Q8AXW1
32 263 32.2 146 13 Q8AXW2
33 261.5 32.0 146 13 Q7T1R1
34 260.5 31.9 146 13 Q8AXW7
35 259.5 31.8 146 13 Q8AY48
36 257 31.5 137 13 Q8AXW0
37 256 31.3 145 13 Q9DEB0
38 254.5 31.2 148 13 Q7T2Q4
39 251 30.7 147 13 Q8WS88
40 239.5 29.3 156 5 Q8WS88
41 232 27.2 147 13 Q7C2Q5
42 216.5 26.5 142 13 Q802I1
43 214 26.2 149 13 Q9YH62
44 212.5 26.0 138 5 Q9U8P8
45 206.5 25.3 149 13 O57313

DR PRINTS; PR00389; PHPLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2c; 1.
DR PROSITE; PS00119; PA2 ASP; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
SQ SEQUENCE 138 AA; 15456 MW; 513647907BFD0F4E CRC64;

Query Match 41.3%; Score 337.5; DB 13; Length 138;
Best Local Similarity 45.3%; Pred. No. 1.3e-30;
Matches 62; Conservative 19; Mismatches 53; Indels 3; Gaps 2;

QY 7 LVFLCLLVALVTGNLVQGVMIKWTGKSA-ALQNDYGCYCGIGGSHWPVDQTDWCCHAH 65
Db 4 LWIMAVLLVGVGSLWQFGKNTYMGESGLVLSYGCYCGIGGSHWPVDQTDWCCHAH 63
QY 66 DCCYGRLEKLGCEPKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRNLTGTYNR 125
Db 64 DCCYGRLEKLGCEPKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRNLTGTYNR 121

QY 126 KYAHYPNKLCTGTPPC 142
Db 122 KYMFGAKNCOEKSEPC 138

RESULT 5
Q805A2
ID Q805A2 PRELIMINARY; PRT; 138 AA.
AC Q805A2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PLA-N(O).
GN PLA2.
OS Trimeresurus flavoviridis (Habu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=88087;
RN [1]
RP SEQUENCE FROM N.A.
RA Chijiwa T., Hamai S., Tsubouchi S., Ogawa T., Deshimaru M.,
RA Oda-Ueda N., Hattori S., Kihara H., Tsunazawa S., Ohno M.;
RT "Interisland mutation of a novel phospholipase A2 from Trimeresurus
RT flavoviridis venom and evolution of crotalinae group II phospholipase
RT A2";
RL Submitted (EBB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB102729; BAC56893.1; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PR00389; PHPLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2c; 1.
DR PROSITE; PS00119; PA2 ASP; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
SQ SEQUENCE 138 AA; 15803 MW; A2F103123897ECC5 CRC64;

Query Match 41.3%; Score 337.5; DB 13; Length 138;
Best Local Similarity 47.4%; Pred. No. 1.3e-30;
Matches 65; Conservative 15; Mismatches 54; Indels 3; Gaps 2;

QY 7 LVFLCLLVALVTGNLVQGVMIKWTGKSAQ-QYNDYGCYCGIGGSHWPVDQTDWCCHAH 65
Db 4 LWIMAVLLVGVGSLWQFGKNTYMGESGLVLSYGCYCGIGGSHWPVDQTDWCCHAH 63
QY 66 DCCYGRLEKLGCEPKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRNLTGTYNR 125
Db 64 DCCYGRLEKLGCEPKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRNLTGTYNR 121

QY 126 KYAHYPNKLCTGTPPC 142

Db 122 KYMFGDFLCTDPTKTC 138

RESULT 6
Q7ZTA8
ID Q7ZTA8 PRELIMINARY; PRT; 138 AA.
AC Q7ZTA8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Acidic phospholipase A2.
OS Crotalus viridis viridis (Prairie rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Crotalus.
OX NCBI_TaxID=8742;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E6b;
RX MEDLINE=22510024; PubMed=12623078;
RA Tsai I.-H., Wang Y.-M., Chen Y.-H., Tu A.T.;
RT "Geographic variations, cloning, and functional analyses of the venom
RT acidic phospholipases A2 of Crotalus viridis viridis";
RL Arch. Biochem. Biophys. 411:289-296(2003).
DR EMBL; AF128875; AAM80563.1; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PR00389; PHPLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2c; 1.
DR PROSITE; PS00119; PA2 ASP; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
SQ SEQUENCE 138 AA; 15414 MW; 44A35EA1FE6A39D0 CRC64;

Query Match 40.5%; Score 330.5; DB 13; Length 138;
Best Local Similarity 45.3%; Pred. No. 9e-30;
Matches 62; Conservative 18; Mismatches 54; Indels 3; Gaps 2;

QY 7 LVFLCLLVALVTGNLVQGVMIKWTGKSA-QYNDYGCYCGIGGSHWPVDQTDWCCHAH 65
Db 4 LWIMAVLLVGVGSLWQFGKNTYMGESGLVLSYGCYCGIGGSHWPVDQTDWCCHAH 63
QY 66 DCCYGRLEKLGCEPKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRNLTGTYNR 125
Db 64 DCCYGRLEKLGCEPKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRNLTGTYNR 121

QY 126 KYAHYPNKLCTGTPPC 142
Db 122 KYMFGAKNCOEKSEPC 138

RESULT 7
Q7ZTA6
ID Q7ZTA6 PRELIMINARY; PRT; 138 AA.
AC Q7ZTA6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Acidic phospholipase A2.
OS Crotalus viridis viridis (Prairie rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Crotalus.
OX NCBI_TaxID=8742;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E6b;
RX MEDLINE=22510024; PubMed=12623078;
RA Tsai I.-H., Wang Y.-M., Chen Y.-H., Tu A.T.;
RT "Geographic variations, cloning, and functional analyses of the venom

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OM protein - protein search, using sw model

Run on: July 3, 2004, 05:12:17 ; Search time 40.1887 Seconds
(without alignments)

998.335 Million cell updates/sec

Title: US-10-088-092a-30

Perfect score: 817

Sequence: 1 MKSPHVLVFLCLVALVTGN.....YNRKYAHYPNKLCTGTPPC 142

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001s.*

5: Geneseq2002s.*

6: Geneseq2003as.*

7: Geneseq2003bs.*

8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	817	100.0	142	4	AAB81022 Human pro
2	817	100.0	154	6	ABR44235 Human sec
3	817	100.0	154	6	ABU63125 Human gro
4	709	86.8	142	3	AAB12810 Mouse sec
5	709	86.8	142	4	AAB81021 Murine ph
6	370	45.3	164	3	AAB56432 Human pro
7	368.5	45.1	144	1	AAP93112 Human inf
8	368.5	45.1	144	1	AAP93363 Human syn
9	368.5	45.1	144	2	AAR25416 PLA2. 1/1
10	368.5	45.1	144	2	AAR63055 Human PLA
11	368.5	45.1	144	6	ABR44233 Human sec
12	368.5	45.1	144	6	ABP96807 Human pro
13	368.5	45.1	144	6	ABU63123 Human gro
14	368.5	45.1	144	7	ADB75501 Prostase
15	368.5	45.1	144	7	ADB75501 Prostase
16	363.5	44.5	124	6	ADA61984 Human I8M
17	360.5	44.1	124	2	AAW10126 Membrane-
18	360.5	44.1	124	2	AAW73562 Human gro
19	360.5	44.1	124	6	ADA61982 Human G72
20	360.5	44.1	124	6	ADA61978 Human G72
21	360.5	44.1	124	6	ABR33569 Human PLA
22	359.5	44.0	146	7	ADA63558 Rat Prote
23	357.5	43.8	124	6	ADA61983 Human T10
24	351	43.0	145	2	AAR63053 HPLA2-8.
25	350	42.8	146	2	AAW08368 Mouse PLA

26	350	42.8	146	5	ABB08154	Ab08154 Murine PL
27	350	42.8	146	6	ABP96808	Abp96808 Mouse pro
28	348	42.6	125	2	AAR63060	Aar63060 Rat PLA2
29	331.5	40.6	122	3	AAV88292	Aay88292 Agkistrod
30	329	40.3	144	3	ABU63126	Aab12536 Mouse sec
31	329	40.3	144	3	ABU63126	Aab11994 Mouse sec
32	317.5	38.9	138	2	AAR63046	Aar63046 HPLA2-10.
33	317.5	38.9	138	6	ABR44237	Abr44237 Human sec
34	317.5	38.9	138	6	ABR44237	Abr44237 Human sec
35	317.5	38.9	138	6	ABU63126	Aae37571 Human pro
36	317.5	38.9	138	7	ADB75501	Abu63126 Human pro
37	317.5	38.9	138	7	ADB75501	Abu63126 Human pro
38	317.5	38.9	138	7	ADB75501	Abu63126 Human pro
39	314.5	38.5	132	2	AAW58476	AAW58476 Human pro
40	314.5	38.5	137	2	AAR63045	Aar63045 HPLA2-10.
41	314.5	38.5	137	7	ADD47917	Add47917 Rat Prote
42	314.5	38.5	137	7	ADD47909	Add47909 Rat Prote
43	314.5	38.5	137	7	ADD47913	Add47913 Rat Prote
44	310.5	38.0	145	4	AAU09096	Aau09096 Novel hum
45	310.5	38.0	145	6	ABR44234	Abr44234 Human sec

ALIGNMENTS

RESULT 1

AAB81022
ID AAB81022 standard; protein; 142 AA.

XX AAB81022;

AC AAB81022;

DT 12-JUN-2001 (first entry)

XX Human phospholipase A2 (PLA2) amino acid sequence.

XX Phospholipase A2; PLA2; antibacterial; immunosuppressive; vulnary;
KW antiinflammatory; tranquiliser; antischmatic; antiallergic; trauma;
KW antirheumatic; antiarthritic; septic shock; pancreatitis; human;
KW adult respiratory distress syndrome; ARDS; bronchial asthma;
KW allergic rhinitis; rheumatoid arthritis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..19

FT Protein /label= Signal_peptide

FT Protein /label= Mature PLA2

FT Protein /note= "Mature phospholipase A2"

FT WO200121775-A1.

XX 29-MAR-2001.

XX 18-SEP-2000; 2000WO-JP006344.

XX 21-SEP-1999; 99JP-00266616.

XX (SHIO) SHIONOGI & CO LTD.

XX Ishizaki J, Suzuki N, Hanasaki K;

XX WPI; 2001-290432/30.

XX N-PSDB; AAF77401.

XX Human secretory phospholipase A2 and encoded gene, useful in diagnosis of

PT and screening drug candidates for treating associated diseases e.g.
PT septic shock, adult respiratory distress syndrome and rheumatoid
PT arthritis.
XX Claim 1; Page 46-47; 50pp; Japanese.
XX This invention relates to human secretory phospholipase A2 (PLA2) protein

CC and the gene encoding it. Inhibitors of phospholipase A2 have
 CC antibacterial; immunosuppressive; antiinflammatory; tranquiliser;
 CC vulnary; antiasthmatic; antiallergic; antirheumatic; and antiarthritic
 CC activity. The PLA2 protein, gene and an anti-PLA2 antibody are useful in
 CC the diagnosis of PLA2 associated diseases e.g. septic shock, adult
 CC respiratory distress syndrome, pancreatitis, trauma, bronchial asthma,
 CC allergic rhinitis and rheumatoid arthritis. The present sequence
 CC represents human PLA2
 XX
 XX Sequence 142 AA;

Query Match 100.0%; Score 817; DB 4; Length 142;
 Best Local Similarity 100.0%; Pred. No. 1.5e-67;
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKSPHVLVFLCLLVALVTGNLVQFGVMIKMTGKSAQYNDYGCYGGSHWPDQTDW 60
 DB 1 MKSPHVLVFLCLLVALVTGNLVQFGVMIKMTGKSAQYNDYGCYGGSHWPDQTDW 60
 QY 61 CCHADCCYGRLEKLGCEPKLEKYLFSVSEGIKMTGKSAQYNDYGCYGGSHWPDQTDW 120
 DB 61 CCHADCCYGRLEKLGCEPKLEKYLFSVSEGIKMTGKSAQYNDYGCYGGSHWPDQTDW 120
 QY 121 GTYRKAYAHYPNKLCTGTPPC 142
 DB 121 GTYRKAYAHYPNKLCTGTPPC 142

RESULT 2
 ABR44235
 ID ABR44235 standard; protein; 154 AA.
 XX ABR44235;
 AC ABR44235;
 DT 18-AUG-2003 (first entry)
 XX Human secreted group IIE phospholipase A2 (sPLA2) enzyme.

DE Group IIF secreted phospholipase A2; sPLA2; phosphatidylglycerol; human;
 KW phosphatidylcholine; antibacterial; virucide; cytostatic; vasotropic;
 KW antiinflammatory; vulnary; cardiac; chromosome lp35; transgenic;
 KW enzyme.
 XX Homo sapiens.
 OS WO2003033689-A1.

XX 24-APR-2003.
 XX 12-OCT-2001; 2001WO-IB002407.
 XX 12-OCT-2001; 2001WO-IB002407.
 XX (CNRS) CNRS CENT NAT RECH SCI.
 XX Lazdunski M, Lambeau G, Valentin E;
 XX WPI; 2003-403216/38.

XX Novel mammalian secreted group IIF secreted phospholipase A2, useful for
 PT preventing and treating bacterial and viral infections, and cancers.
 XX Disclosure; Fig 1; 33pp; English.

XX The invention relates to a mammalian secreted group IIF secreted
 CC phospholipase A2 (sPLA2) (I), where the enzyme is Ca²⁺ dependent,
 CC maximally active at pH 7-8 and hydrolyzes phosphatidylglycerol versus
 CC phosphatidylcholine with a 15-fold preference. A pharmaceutical
 CC composition comprising (I) is useful for treating or preventing viral and
 CC bacterial infections, and cancers. A pharmaceutical composition
 CC containing compounds capable of inhibiting catalytic activity of (I).
 CC biologically active compounds that bind sPLA2 receptors, or a compound
 CC that modulates cell proliferation, cell migration, cell contraction or

CC apoptosis is useful for treating disease states or disorders involving
 CC group IIF sPLA2, such as inflammatory disease, cancers, cardiac and brain
 CC ischaemia, acute lung injury, acute respiratory distress syndrome or
 CC Crohn's disease. Specific antibodies are useful for searching new
 CC secreted mammalian group IIF sPLA2 or the homologues of the enzyme in
 CC other mammals. The encoding polynucleotides and vectors are useful for
 CC transforming animals and establishing a line of transgenic animals.
 CC Sequences ABR44232-238 represent various human secreted sPLA2 enzymes
 CC used in alignment studies with the GIIIF sPLA2 enzyme
 XX
 XX Sequence 154 AA;

Query Match 100.0%; Score 817; DB 6; Length 154;
 Best Local Similarity 100.0%; Pred. No. 1.6e-67;
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKSPHVLVFLCLLVALVTGNLVQFGVMIKMTGKSAQYNDYGCYGGSHWPDQTDW 60
 DB 13 MKSPHVLVFLCLLVALVTGNLVQFGVMIKMTGKSAQYNDYGCYGGSHWPDQTDW 72
 QY 61 CCHADCCYGRLEKLGCEPKLEKYLFSVSEGIKMTGKSAQYNDYGCYGGSHWPDQTDW 120
 DB 73 CCHADCCYGRLEKLGCEPKLEKYLFSVSEGIKMTGKSAQYNDYGCYGGSHWPDQTDW 132
 QY 121 GTYRKAYAHYPNKLCTGTPPC 142
 DB 133 GTYRKAYAHYPNKLCTGTPPC 154

RESULT 3
 ABR63125
 ID ABR63125 standard; protein; 154 AA.
 XX ABR63125;
 AC ABR63125;
 DT 25-SEP-2003 (first entry)
 XX Human group IIE secreted phospholipase A2.

DE Human; group IIE secreted phospholipase A2; virucide; antibacterial;
 KW cytostatic; antiinflammatory; vasotropic; cerebroprotective; sPLA2;
 KW phosphatidylglycerol hydrolysis; phosphatidylcholine hydrolysis;
 KW viral infection; bacterial infection; cancer; inflammatory disease;
 KW cardiac ischaemia; brain ischaemia; acute lung injury;
 KW acute respiratory distress syndrome; Crohn's disease; enzyme.

XX Homo sapiens.
 OS US2003073087-A1.
 XX 17-APR-2003.
 XX 11-OCT-2001; 2001US-00975456.
 XX 11-OCT-2000; 2000US-0239491P.
 XX (LAZD/) LAZDUNSKI M.
 XX (LAMB/) LAMBEAU G.
 XX (VALE/) VALENTIN E.
 XX Lazdunski M, Lambeau G, Valentin E;
 XX WPI; 2003-567302/53.

XX New mammalian secreted group IIF phospholipase A2 or nucleic acid, useful
 PT for treating or preventing viral or bacterial infections, or cancers, or
 PT screening inhibitors of the enzyme for treating e.g. inflammatory
 PT diseases or ischemia.
 XX Disclosure; Fig 1; 16pp; English.
 XX The invention describes a mammalian secreted group IIF phospholipase A2
 CC (sPLA2), which is Ca²⁺-dependent, maximally active at pH of about 7-8,

CC and hydrolyses phosphatidylglycerol versus phosphatidylcholine with about
CC a 15-fold preference. The mammalian secreted group IIP sPLA2 protein or
CC nucleic acid, or a pharmaceutical composition is useful for treating
CC and/or preventing viral infections, bacterial infections, or cancers. The
CC inhibitors of sPLA2 or a composition comprising sPLA2 inhibitors is
CC useful for treating disease states or disorders involving group IIF
CC sPLA2, e.g. inflammatory diseases, cancer, cardiac and brain ischaemia,
CC acute lung injury, acute respiratory distress syndrome, or Crohn's
CC disease. The enzyme is also useful for screening various chemical
CC compounds for treating these diseases. This is the amino acid sequence of
CC human group IIE phospholipase A2 used to determine a consensus sequence
CC for human sPLA2s

XX Sequence 154 AA;

Query Match 100.0%; Score 817; DB 6; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.6e-67;
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKSPHVLVFLCLLVALVTGNLVQFGVMIEKMTGKSAQYNDYGCYCGIGGSHWPVDQTDW 60
DB 13 MKSPHVLVFLCLLVALVTGNLVQFGVMIEKMTGKSAQYNDYGCYCGIGGSHWPVDQTDW 72
QY 61 CCHAHDCYGRLEKLGCEPKLEKLFVSERGIFCAGRTTCQRLTCECDKRAALCFRRNL 120
DB 73 CCHAHDCYGRLEKLGCEPKLEKLFVSERGIFCAGRTTCQRLTCECDKRAALCFRRNL 132
QY 121 GTYNRYAHYPNKLCTGTPPPC 142
DB 133 GTYNRYAHYPNKLCTGTPPPC 154

RESULT 4

AAB12810
ID AAB12810 standard; protein; 142 AA.

AC AAB12810;

DT 27-NOV-2000 (first entry)

XX Mouse secretory type phospholipase A2 protein SEQ ID NO:15.

XX Mouse; secretory phospholipase A2; PLA2; screening; development;
XX inhibitor.

XX Mus musculus.

XX JP2000166568-A.

XX 20-JUN-2000.

XX 09-DEC-1998; 98JP-00349604.

XX 09-DEC-1998; 98JP-00349604.

XX (SHIO) SHIONOGI & CO LTD.

XX WPI; 2000-485554/43.

XX N-PSDB; AAA73130.

XX New gene encoding mouse secretory type phospholipase A2 (PLA2) for
XX screening for inhibitors of PLA2.

XX Claim 1; Page 13-14; 15pp; Japanese.

XX The present invention describes a mouse secretory type phospholipase A2
XX (PLA2) protein. The mouse secretory type PLA2-like protein can be used
XX for screening in the development of inhibitors against the function of
XX the protein. The present sequence represents mouse secretory type PLA2

SQ Sequence 142 AA;

Query Match

86.8%; Score 709; DB 3; Length 142;

Best Local Similarity 84.5%; Pred. No. 1.3e-57;
Matches 120; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 MKSPHVLVFLCLLVALVTGNLVQFGVMIEKMTGKSAQYNDYGCYCGIGGSHWPVDQTDW 60
DB 1 MKPPIALACLCILVPLAGGNLVQFGVMIEKMTGKSAQYNDYGCYCGIGGSHWPVDQTDW 60

QY 61 CCHAHDCYGRLEKLGCEPKLEKLFVSERGIFCAGRTTCQRLTCECDKRAALCFRRNL 120

DB 61 CCHAHDCYGRLEKLGCEPKLEKLFVSITRDNIFCAGRTACQRTCECDKRAALCFRRNL 120

QY 121 GTYNRYAHYPNKLCTGTPPPC 142

DB 121 NTYNRYAHYPNKLCTGTPPPC 142

RESULT 5

AAB81021

ID AAB81021 standard; protein; 142 AA.

AC AAB81021;

DT 12-JUN-2001 (first entry)

XX Murine phospholipase A2 (PLA2) amino acid sequence.

XX Phospholipase A2; PLA2; antibacterial; immunosuppressive; vulnery;
XX antiinflammatory; tranquiliser; antialsthetic; antiallergic; trauma;
XX antirheumatic; antiarthritic; septic shock; pancreatitis; mouse;
XX adult respiratory distress syndrome; ARDS; bronchial asthma;
XX allergic rhinitis; rheumatoid arthritis.

XX Mus musculus.

XX Key Location/Qualifiers

FT Peptide 1..19

FT Protein /label= Signal_peptide

FT /label= Mature_PLA2

FT /note= "Mature phospholipase A2"

PN WO200121775-A1.

XX 29-MAR-2001.

XX 18-SEP-2000; 2000WO-JP006344.

XX 21-SEP-1999; 99JP-00266616.

XX (SHIO) SHIONOGI & CO LTD.

XX Ishizaki J, Suzuki N, Hanasaki K;

XX WPI; 2001-290432/30.

XX N-PSDB; AAF77387.

XX Human secretory phospholipase A2 and encoded gene, useful in diagnosis of
XX and screening drug candidates for treating associated diseases e.g.
XX septic shock, adult respiratory distress syndrome and rheumatoid
XX arthritis.

XX Example 3; Page 42; 50pp; Japanese.

XX This invention relates to human secretory phospholipase A2 (PLA2) protein
XX and the gene encoding it. Inhibitors of phospholipase A2 have
XX antibacterial; immunosuppressive; antiinflammatory; tranquiliser;
XX vulnery; antialsthetic; antiallergic; antirheumatic; and antiarthritic
XX activity. The PLA2 protein, gene and an anti-PLA2 antibody are useful in
XX the diagnosis of PLA2 associated diseases e.g. septic shock, adult
XX respiratory distress syndrome, pancreatitis, trauma, bronchial asthma,
XX allergic rhinitis and rheumatoid arthritis. The present sequence
XX represents murine PLA2. The murine PLA2 gene sequence is used in the
XX invention for the identification and characterisation of the human PLA2

(BIOL) BIOGEN INC.

Kramer RM, Pepinsky R, Hession C;
WPI; 1989-324225/44.
N-PSDB; AAN91825, AAN97209.

Acid stable phospholipase A2 - used for prodn. of antibodies and in the treatment or diagnosis of inflammation and other diseases.

Claim 44; Fig 12; 84pp; English.

The protein sequence was deduced from a DNA sequence obtd. from a genomic DNA library which was prep'd from a mutant fibroblast cell line which contains 5 copies of the X chromosome (GM5009). The signal sequence is thought to be incomplete at the N-terminal since no promoter-like sequences are found in the DNA within 100 nucleotides 5' of this region. The deduced N-terminal sequence of the mature protein confirmed results obtd. by direct sequencing of the purified protein. This sequence represents an amphiphilic alpha-helix typical of PLA 2 mols. It has highly conserved lipophilic residues (e.g. Leu (22), Phe (25), and Ile (29)) and there is a cluster of basic amino acids (e.g. Arg (27), Lys (30) and Lys (35)) which is believed to be an important determinant in the interaction of PLA2. There is a characteristic stretch of residues which comprises part of the calcium binding loop: Tyr(44)-Gly-Cys-X-Cys-Gly-X-Gly-Gly-X-X-Pro(56) and Asp(68). The conserved residues which constitute the active site (see features) are also present, and the protein exhibits the placement of half-cysteine residues typical of a Gp II PLA2, having a Cys residue at position 70 and a half cysteine at the C-terminal. (The consensus sequence was determined from a comparison of PLA2s from bovine pancreas and C. atrox venom. (Updated on 25-MAR-2003 to correct PR field.)

XX -
SQ Sequence 144 AA;

Query Match 45.1%; Score 368.5; DB 1; Length 144;
Best Local Similarity 52.1%; Pred. No. 3.2e-26;
Matches 73; Conservative 12; Mismatches 46; Indels 9; Gaps 2;

QY 12 LLVALVT-----GNLVQGVMIKMTGK-SALQYNDYGCYIGGSHWPVDQTDWCC 62
DB 5 LLLAVIMIFGLLAQHGNLWVFMHMKLTGKRAALSYGYCHGCVGRGSPKDATDRCC 64
QY 63 HAHDCCYGRLEKLGCEPKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRRNLGT 122
DB 65 VTHDCCYKLEKRGCGTKFLSYKFSNRSRITCAKQDSCRSQLCECDKAAATCFARNKTT 124
QY 123 YNRKYAHYFNKLCGTPTPC 142
DB 125 YNKYQYYSNKHCRGSTPRC 144

RESULT 8
AAP93363
ID AAP93363 standard; protein; 144 AA.
AAP93363;
XX
AC AAP93363;
XX
DT 25-MAR-2003 (revised)
DT 27-JUN-1980 (first entry)
XX
DE Human synovial phospholipase type A2 (sPLA2) as encoded by cDNA clone
DE lambda sPLA2cDNA-4 and by the exons of clone lambda sPLA2-6.
KW Human synovial phospholipase A2; clone lambda sPLA2cDNA-4;
KW lambda sPLA2-6.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Protein 21..144
XX
DN WO8901773-A.

09-MAR-1989.
23-AUG-1988; 88WO-US002896.
27-AUG-1987; 87US-00089883.
06-JUL-1988; 88US-00215726.
16-AUG-1988; 88US-00231865.
(BIOT-) BIOTECHN RES PARTN.
(UTOR) UNIV OF TORONTO INNOVAT.

Johnson LX, Seilhamer JJ, Pruzanski W, Vadas P;
WPI; 1989-085394/11.
N-PSDB; AAN91258, AAN91260.

Mammalian synovial phospholipase A2 - used in food processing, design and screening of inflammation inhibitors, as an anticancer drug or vaccine adjuvant etc.

Disclosure; Fig 6; 70pp; English.

Clone lambda sPLA2cDNA-4 is one of four clones identified when probe oligo 2905 (AAN91257) was used to screen a cDNA library constructed from polyA+ message from a peritoneal cell RNA. It encodes the entire sPLA2 type A sequence which is given here. The mature peptide sequence (see FT) has a calculated molecular weight of 13,919 daltons. The same amino acid sequence is also encoded by the exons of clone lambda sPLA2-6 (AAN91260) in Figure 7. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)

XX
SQ Sequence 144 AA;

Query Match 45.1%; Score 368.5; DB 1; Length 144;
Best Local Similarity 52.1%; Pred. No. 3.2e-26;
Matches 73; Conservative 12; Mismatches 46; Indels 9; Gaps 2;

QY 12 LLVALVT-----GNLVQGVMIKMTGK-SALQYNDYGCYIGGSHWPVDQTDWCC 62
DB 5 LLLAVIMIFGLLAQHGNLWVFMHMKLTGKRAALSYGYCHGCVGRGSPKDATDRCC 64
QY 63 HAHDCCYGRLEKLGCEPKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRRNLGT 122
DB 65 VTHDCCYKLEKRGCGTKFLSYKFSNRSRITCAKQDSCRSQLCECDKAAATCFARNKTT 124
QY 123 YNRKYAHYFNKLCGTPTPC 142
DB 125 YNKYQYYSNKHCRGSTPRC 144

RESULT 9
AAR25416
ID AAR25416 standard; protein; 144 AA.
XX
AC AAR25416;
XX
DT 06-JAN-1993 (first entry)
XX
DE PLA2.
XX
KW Human growth hormone; granulocyte-colony stimulating factor; G-CSF;
KW phospholipase A2; HGH; PCR; polymerase chain reaction; gene therapy;
KW erythroid cells; cDNA library.
XX
OS Synthetic.
XX
PN GB2251622-A.
XX
PD 15-JUL-1992.
XX
PF 19-DEC-1991; 91GB-00026984.

XX 21-DEC-1990; 90GB-00027917.
PR (ICIL) IMPERIAL CHEM IND PLC.
XX Hollis M, Needham MRC, Gooding C, Grosveld FG, Antoniou M;
XX WPI; 1992-236158/29.
XX N-PSDB; AAQ26372.
XX
XX Expression vectors for use in mammalian cells - contain dominant control
PT region derived from beta-globin gene.
XX
XX Disclosure; Fig 11; 77pp; English.
XX
XX This sequence is encoded by the phospholipase A2 (PLA2) cDNA. The cDNA
XX was amplified using the primer sequences given in AAQ26370-1 by PCR from
XX a human lung cDNA library. The cDNA sequence was used in the construction
XX of an expression vector which further comprised a promoter and a dominant
XX control region. This vector was used in an expression system comprising a
XX mammalian cell transformed with the vector. This expression system could
XX be used to prepare pharmacologically useful polypeptides eg. human growth
XX hormone (hGH), granulocyte-colony stimulating factor (G-CSF) and PLA2,
XX and for gene therapy. The mammalian host comprises erythroid cells and a
XX heterologous promoter
XX
XX Sequence 144 AA;
XX
XX Query Match 45.1%; Score 368.5; DB 2; Length 144;
XX Best Local Similarity 52.1%; Pred. No. 3.2e-26;
XX Matches 73; Conservative 12; Mismatches 46; Indels 9; Gaps 2
XX
XX QY 12 LLAVALVT-----GNLVQFGVMIEKMTGK-SALQYNDYGCYCGIGGSHWPVDQTDWCC 62
XX DB 5 LLLAVIMIFGLLOAHGNLVNFRHMLKLTGKEAALSYGFGYCHGCVGRGSPKDATDRCC 64
XX
XX QY 63 HAHDCCYGRLEKGLCEPKLEKYLFSVBERGIFCAGRTTCORLTCECDKKAALCFRRNLGT 122
XX DB 65 VTHDCYKRLKRGKGCTGTFSLYKFSNSGSRITCAKQDCSRSQLCECDKAAATCFARNKTT 124
XX
XX QY 123 YNRKYAHYENKLCGTGTPPC 142
XX DB 125 YNRKYQYYSNKHCRGSTRC 144
XX
XX
XX RESULT 10
XX AAR63055
XX ID AAR63055 standard; protein; 144 AA.
XX AC AAR63055;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 15-AUG-1995 (first entry)
XX
XX DE Human PLA2 type II.
XX
XX HPLA2-10; phospholipase A2; PLA2.
XX
XX Homo sapiens.
XX
XX WO9502328-A1.
XX
XX 26-JAN-1995.
XX
XX 15-JUL-1994; 94WO-US007926.
XX
XX 15-JUL-1993; 93US-00091941.
XX 26-JUL-1993; 93US-00097354.
XX
XX (INDV) UNIV INDIANA FOUND.
XX (INCY-) INCYTE PHARM INC.
XX
XX Tischfield JA, Seilhamer JJ;
XX

phosphatidylcholine with a 15-fold preference. A pharmaceutical composition comprising (I) is useful for treating or preventing viral and bacterial infections, and cancers. A pharmaceutical composition containing compounds capable of inhibiting catalytic activity of (I), biologically active compounds that bind sPLA₂ receptors, or a compound that modulates cell proliferation, cell migration, cell contraction or apoptosis is useful for treating disease states or disorders involving group IIF sPLA₂, such as inflammatory disease, cancers, cardiac and brain ischaemia, acute lung injury, acute respiratory distress syndrome or Crohn's disease. Specific antibodies are useful for searching new secreted mammalian group IIF sPLA₂ or the homologues of the enzyme in other mammals. The encoding polynucleotides and vectors are useful for transforming animals and establishing a line of transgenic animals. Sequences AB44232-238 represent various human secreted sPLA₂ enzymes used in alignment studies with the G1F sPLA₂ enzyme

XX Sequence 144 AA;

Query Match 45.1%; Score 368.5; DB 6; Length 144;
Best Local Similarity 52.1%; Pred. No. 3.2e-26;
Matches 73; Conservative 12; Mismatches 46; Indels 9; Gaps 2;
QY 12 LLVALVT-----GNLVQGVMIKMTGK-SALQVNDYGCYGGSHWPVDQTDWCC 62
DB 5 LLLAVIMIFGLLOAHGNLVNFRHMIKLTGKEAALSIFYGCHGVGSGSPKDATDRCC 64
QY 63 HAHDCCYGRLEKGECEPKLEKYLFSVBERGIFCAGRTTCORLTCCDRAALCFRRNLGT 122
DB 65 VTHDCCYKRLKRGCGTKFLSYKFSNSGRITCAKQDSCRQSCDCAAAATCFARNKTT 124
QY 123 YNRKYAHYPNKLCTGTPPC 142
DB 125 YNKYQYYSNKHCRGSTPRC 144

RESULT 12
ABP96807
ID ABP96807 standard; protein; 144 AA.

AC ABP96807;
XX 05-JUN-2003 (first entry)
XX Human phospholipase A2 group IIA (synovial) SEQ ID NO:3.
XX
XX Phospholipase A2 group IIA; synovial; antisense modulation; inflammation;
XX phospholipase A2 group IIA inhibitor; phosphorothioate; antiinflammatory;
XX antidiabetic; cytostatic; antipsoriatic; vaccine; gene therapy; cancer;
XX psoriasis; diabetes; enzyme.
XX Homo sapiens.
XX WO200297133-A1.
XX
XX 05-DEC-2002.
XX
XX 21-MAY-2002; 2002WO-US016135.
XX
XX 25-MAY-2001; 2001US-00865866.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Wyatt JR;
XX WPI; 2003-140495/13.
XX N-PSDB; ACC46906, ACC46921.
XX
XX New compound that hybridizes with and inhibits the expression of
XX Phospholipase A2, group IIA, useful for preparing a composition for
XX treating or preventing inflammation, cancer, psoriasis or diabetes.
XX Example 13; Page 95-96; 135pp; English.

CC The present invention describes a compound (I) comprising 8-50
CC nucleobases which is targeted to a 5' untranslated region (UTR), coding,
CC 3' UTR or intron region of a nucleic acid molecule encoding phospholipase
CC A2, group IIA (synovial), where the compound specifically hybridizes with
CC and inhibits the expression of phospholipase A2, group IIA (synovial).
CC Also described: (1) a composition comprising the compound and a carrier
CC or diluent; (2) a method of inhibiting the expression of phospholipase
CC A2, group IIA in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with phospholipase A2, group IIA
CC (synovial). (1) has antiinflammatory, antidiabetic, cytostatic and
CC antipsoriatic activities, and can be used in vaccines and in gene
CC therapy. The compound (I) can be used for preparing a composition for
CC treating or preventing inflammation, cancer, psoriasis or diabetes. The
CC present sequence represents human phospholipase A2 group IIA (synovial),
CC which is used in an example from the present invention
XX
XX Sequence 144 AA;

Query Match 45.1%; Score 368.5; DB 6; Length 144;
Best Local Similarity 52.1%; Pred. No. 3.2e-26;
Matches 73; Conservative 12; Mismatches 46; Indels 9; Gaps 2;
QY 12 LLVALVT-----GNLVQGVMIKMTGK-SALQVNDYGCYGGSHWPVDQTDWCC 62
DB 5 LLLAVIMIFGLLOAHGNLVNFRHMIKLTGKEAALSIFYGCHGVGSGSPKDATDRCC 64
QY 63 HAHDCCYGRLEKGECEPKLEKYLFSVBERGIFCAGRTTCORLTCCDRAALCFRRNLGT 122
DB 65 VTHDCCYKRLKRGCGTKFLSYKFSNSGRITCAKQDSCRQSCDCAAAATCFARNKTT 124
QY 123 YNRKYAHYPNKLCTGTPPC 142
DB 125 YNKYQYYSNKHCRGSTPRC 144

RESULT 13
ABU63123
ID ABU63123 standard; protein; 144 AA.

AC ABU63123;
XX 25-SEP-2003 (first entry)
XX Human group IIA secreted phospholipase A2.
XX
XX Human; group IIA secreted phospholipase A2; virucide; antibacterial;
XX cytostatic; antiinflammatory; vasotropic; cerebroprotective; sPLA₂;
XX phosphatidylglycerol hydrolysis; phosphatidylcholine hydrolysis;
XX viral infection; bacterial infection; cancer; inflammatory disease;
XX cardiac ischaemia; brain ischaemia; acute lung injury;
XX acute respiratory distress syndrome; Crohn's disease; enzyme.
XX Homo sapiens.
XX US2003073087-A1.
XX
XX 17-APR-2003.
XX
XX 11-OCT-2001; 2001US-00975456.
XX
XX 11-OCT-2000; 2000US-0239491P.
XX (LAZD/) LAZDUNSKI M.
XX (LAMB/) LAMBEAU G.
XX (VALE/) VALENTIN E.
XX
XX Lazdunski M, Lambeau G, Valentin E;
XX WPI; 2003-567302/53.
XX
XX New mammalian secreted group IIF phospholipase A2 or nucleic acid, useful
XX for treating or preventing viral or bacterial infections, or cancers, or
XX screening inhibitors of the enzyme for treating e.g. inflammatory

preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

SQ - Sequence 144 AA;

Query Match	45.1%	Score	368.5;	DB	7;	Length	144;
Best Local Similarity	52.1%;	Pred. No.	3.2e-26;				
Matches	73;	Conservative	12;	Mismatches	46;	Indels	9; Gaps
QY	12	LLVALVT-----GNLVQGVGVIKMTGK-SALQVNDYGCYCIGTGGSHWPVDQTDDCC	62				
		:::					
Ddb	5	LLLAVINIFGLQAAGNLVNFRHMIKLTTGKEAALSIFYGCHCGVGGRSPXDAIDRCC	64				
		:::					
QY	63	HAHDCCYGRLEKLGCEPKLEYLFSVSERIGFCAGRITTCORLTCECDKRAALCFRRNLGT	122				
		:::					
Ddb	65	VTHDCCYKRLEKEGCGTKFLSYKFNSSGSRICTAKQDSCHSOLCEDKAATCAFNKIT	124				
		:::					
QY	123	YNRYAHYHNKLCGTGTPPC	142				
		:::					
Ddb	125	YNKKYQIYSNKHCRGSTPRC	144				
		:::					

Search completed: July 3, 2004, 05:16:16
Job time : 43.1887 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 3, 2004, 05:14:29 ; Search time 10.6755 Seconds
(without alignments)
1108.294 Million cell updates/sec

Title: US-10-088-092A-30_COPY_20_142

Perfect score: 722

Sequence: 1 NLVQGVMIKMTGKSALOY.....YNRKYAHYFNKLTGTPPC 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:**
1: PIR1:**
2: PIR2:**
3: PIR3:**
4: PIR4:**

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	372	51.5	121	2	S17860 phospholipase A2 (
2	360.5	49.9	144	1	PSHUFF phospholipase A2 (
3	358.5	49.7	120	2	S13019 phospholipase A2 (
4	358	49.6	137	2	S22388 phospholipase A2 (
5	350	48.5	123	2	B53872 phospholipase A2 (
6	347	48.1	146	2	A33394 phospholipase A2 (
7	340	47.1	121	1	PSBGAC phospholipase A2 (
8	339.5	47.0	122	1	PSVYXF phospholipase A2 (
9	339.5	47.0	138	2	JC1342 phospholipase A2 (
10	337	46.7	146	2	A35493 phospholipase A2 (
11	335.5	46.5	138	2	I50098 phospholipase A2 (
12	335	46.4	146	2	I48342 phospholipase A2 (
13	333.5	46.2	122	2	A25806 phospholipase A2 (
14	333.5	46.2	138	2	S10333 phospholipase A2 (
15	333	46.1	146	2	JU0283 ammodoxylin B prec
16	332.5	46.1	122	2	A33317 phospholipase A2 (
17	332.5	46.1	122	2	S33267 phospholipase A2 (
18	330.5	45.8	138	1	PSVIAA phospholipase A2 (
19	330.5	45.8	138	1	PSVIAC phospholipase A2 (
20	330.5	45.8	138	2	I51190 phospholipase A2 (
21	330	45.7	124	2	I51190 phospholipase A2 (
22	329.5	45.6	122	2	A44179 phospholipase A2 (
23	328.5	45.5	122	1	PSABA phospholipase A2 (
24	326.5	45.2	138	2	S95922 phospholipase A2 (
25	325.5	45.1	121	2	S17861 phospholipase A2 (
26	325.5	45.1	138	2	F48188 phospholipase A2 (
27	324.5	44.9	122	2	A33872 phospholipase A2 (
28	324.5	44.9	122	2	A37478 phospholipase A2 (
29	324	44.9	145	2	I48093 phospholipase A2 (

RESULT 1
S17860 phospholipase A2 (EC 3.1.1.4) isoform A1 - leaf-nosed viper
C:Species: Eristocophis macmahoni (leaf-nosed viper)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C:Accession: S17860
R:Siddiqi, A.R.; Zaidi, Z.H.; Joernvall, H.
Eur. J. Biochem. 201, 675-679, 1991
A:Title: Purification and characterization of two highly different group II phospholipase
A:Reference number: S17860; MUID:92037623; PMID:1935962
A:Accession: S17860
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-121 <SID>
C:Superfamily: phospholipase A2
C:Keywords: carboxylic ester hydrolase

Query Match 51.5%; Score 372; DB 2; Length 121;
Best Local Similarity 56.5%; Pred. NO. 5e-29;
Matches 70; Conservative 8; Mismatches 42; Indels 4; Gaps 3;

QY	1	NLVQGVMIKMTGKSA-LQYNDYGCYCGIGSGSHWPVDQTCCHAHDCYGRLEKLCGE	59
DB	1	NLYQGRMIFKMTGKSALLSYDYCYGSGKGPLDTRCCFVHDCCYGRVN--GCN	58
QY	60	PKLEYLFSVSERGIFCAGRTTCQRLTCECDKRALCFRRNLGTYNRYAHYFNKLTGTP	119
DB	59	PKLSTYSYSFQNGDIVCGDDNACLRAVCECDRVAICFGENLTYDRKYDYPSSQCT-E	117
QY	120	TPPC	123
DB	118	TEQC	121

ALIGNMENTS

RESULT 1

S17860 phospholipase A2 (EC 3.1.1.4) isoform A1 - leaf-nosed viper
C:Species: Eristocophis macmahoni (leaf-nosed viper)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C:Accession: S17860
R:Siddiqi, A.R.; Zaidi, Z.H.; Joernvall, H.
Eur. J. Biochem. 201, 675-679, 1991
A:Title: Purification and characterization of two highly different group II phospholipase
A:Reference number: S17860; MUID:92037623; PMID:1935962
A:Accession: S17860
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-121 <SID>
C:Superfamily: phospholipase A2
C:Keywords: carboxylic ester hydrolase

Query Match 51.5%; Score 372; DB 2; Length 121;
Best Local Similarity 56.5%; Pred. NO. 5e-29;
Matches 70; Conservative 8; Mismatches 42; Indels 4; Gaps 3;

QY	1	NLVQGVMIKMTGKSA-LQYNDYGCYCGIGSGSHWPVDQTCCHAHDCYGRLEKLCGE	59
DB	1	NLYQGRMIFKMTGKSALLSYDYCYGSGKGPLDTRCCFVHDCCYGRVN--GCN	58
QY	60	PKLEYLFSVSERGIFCAGRTTCQRLTCECDKRALCFRRNLGTYNRYAHYFNKLTGTP	119
DB	59	PKLSTYSYSFQNGDIVCGDDNACLRAVCECDRVAICFGENLTYDRKYDYPSSQCT-E	117
QY	120	TPPC	123
DB	118	TEQC	121

RESULT 2

PSHUFF phospholipase A2 (EC 3.1.1.4) IIA precursor [validated] - human
N:Alternate names: phosphatidylcholine 2-acylhydrolase; placental pIA2; platelet-secretor
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 15-Sep-2000
C:Accession: A32862; B32862; A60266; A32847; A60263; A31350; PT0056; A32913; A60265; A611
R:Kramer, R.M.; Hession, C.; Johansen, B.; Hayes, G.; McGray, P.; Chow, E.P.; Tizard, R.;
J. Biol. Chem. 264, 5768-5775, 1989
A:Title: Structure and properties of a human non-pancreatic phospholipase A-2.
A:Reference number: A32862; MUID:89174633; PMID:2925633
A:Accession: A32862
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-144 <KRA>
A:Accession: B32862
A:Molecule type: protein
A:Residues: 21-39 <KR2>

A;Note: this protein was also detected in platelets
 R;Kramer, R.M.; Johansen, B.; Hession, C.; Pepinsky, R.B.
 Adv. Exp. Med. Biol. 275, 35-53, 1990
 A;Title: Structure and properties of a secretable phospholipase A-2 from human platelets
 A;Reference number: A60266; MUID:91050834; PMID:2239446
 A;Accession: A60266
 A;Status: not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-144 <CR3>
 R;Seilhamer, J.J.; Kruszanski, W.; Vadas, P.; Plant, S.; Miller, J.A.; Kloss, J.; Johnson
 J. Biol. Chem. 264, 5335-5338, 1989
 A;Title: Cloning and recombinant expression of phospholipase A-2 present in rheumatoid a
 A;Reference number: A32847; MUID:89174566; PMID:2925608
 A;Accession: A32847
 A;Molecule type: mRNA
 A;Residues: 1-144 <SBI>
 A;Cross-references: GB:J04704; EMBL:M22430; NID:g190888; PIDN:AAA36550.1; PID:g190889
 R;Crowl, R.; Stoner, C.; Stollner, T.; Pan, Y.C.; Conroy, R.
 Adv. Exp. Med. Biol. 279, 173-184, 1990
 A;Title: Isolation and characterization of cDNA clones from human placenta coding for ph
 A;Reference number: A60263; MUID:91263879; PMID:1710870
 A;Accession: A60263
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-144 <CR0>
 R;Lai, C.Y.; Wada, K.
 Biochem. Biophys. Res. Commun. 157, 488-493, 1988
 A;Title: Phospholipase A-2 from human synovial fluid: purification and structural homolo
 A;Reference number: A31350; MUID:89076274; PMID:3202859
 A;Accession: A31350
 A;Molecule type: protein
 A;Residues: 21-33 <LAI>
 R;Hara, S.; Kudo, I.; Matsuta, K.; Miyamoto, T.; Inoue, K.
 J. Biochem. 104, 326-328, 1988
 A;Title: Amino acid composition and NH2-terminal amino acid sequence of human phospholip
 A;Reference number: PT0056; MUID:89197814; PMID:3240982
 A;Accession: PT0056
 A;Molecule type: protein
 A;Residues: 21-46, 'X', 48-54 <HAR>
 R;Kanda, A.; Ono, T.; Yoshida, N.; Tojo, H.; Okamoto, M.
 Biochem. Biophys. Res. Commun. 163, 42-48, 1989
 A;Title: The primary structure of a membrane-associated phospholipase A-2 from human spl
 A;Reference number: A32913; MUID:89374261; PMID:2775276
 A;Accession: A32913
 A;Molecule type: protein
 A;Residues: 21-144 <KAN>
 R;Parks, T.P.; Lukas, S.; Hoffman, A.F.
 Adv. Exp. Med. Biol. 275, 55-81, 1990
 A;Title: Purification and characterization of a phospholipase A-2 from human osteoarthri
 A;Reference number: A60265; MUID:91050835; PMID:2146857
 A;Accession: A60265
 A;Molecule type: protein
 A;Residues: 21-45, 'X' <PAR>
 R;Recklies, A.D.; White, C.
 Arthritis Rheum. 34, 1106-1115, 1991
 A;Title: Phospholipase A-2 is a major component of the salt-extractable pool of matrix p
 A;Reference number: A61201; MUID:92029121; PMID:1930329
 A;Accession: A61201
 A;Molecule type: protein
 A;Residues: 21-40 <REC>
 R;Green, J.A.; Smith, G.M.; Buchta, R.; Lee, R.; Ho, K.Y.; Rajkovic, I.A.; Scott, K.P.
 Inflammation 15, 355-366, 1991
 A;Title: Circulating phospholipase A-2 activity associated with sepsis and septic shock
 A;Reference number: A61634; MUID:92098137; PMID:1757123
 A;Accession: A61634
 A;Molecule type: protein
 A;Residues: 21-44 <GRE>
 R;Wery, J.P.; Schevitz, R.W.; Clawson, D.K.; Bobbitt, J.L.; Dow, E.R.; Gamboa, G.; Goods
 Teater, C.; Warrick, M.W.; Jones, N.D.
 submitted to the Brookhaven Protein Data Bank, May 1992
 A;Reference number: A51043; PDB:1BBC
 A;Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 21-144

R;Wery, J.P.; Schevitz, R.W.; Clawson, D.K.; Bobbitt, J.L.; Dow, E.R.; Gamboa, G.; Goods
 Teater, C.; Warrick, M.W.; Jones, N.D.
 Nature 352, 79-82, 1991
 A;Title: Structure of recombinant human rheumatoid arthritic synovial fluid phospholipase
 A;Reference number: A58514; MUID:91287826; PMID:2062381
 A;Contents: annotation; X-ray crystallography
 C;Genetics: PLA2G2A; PLA2B; PLA2L
 A;Gene: GDB:PLA2G2A; PLA2B; PLA2L
 A;Cross-references: GDB:120296; OMIM:172411
 A;Map position: 1p36.1-1p35
 A;Introns: 14/1; 62/2; 98/1
 C;Function:

A;Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-acyl-
 A;Note: the reaction is strongly enhanced when the phospholipid is condensed into a micel
 C;Superfamily: phospholipase A2
 C;Keywords: calcium; carboxylic ester hydrolase; extracellular protein; lipid degradatio
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-144/Product: phospholipase A2 IIA #status experimental <MAT>
 F;46-137/48-64,63-117,69-144,70-110,79-103,97-108/disulfide bonds: #status experimental
 F;47,49,51,68/Binding site: calcium (His, Gly, Asp) #status predicted
 F;67,111/Active site: His, Asp #status predicted

Query Match 49.9%; Score 360.5; DB 1; Length 144;
 Best Local Similarity 55.6%; Pred. No. 7.6e-28;
 Matches 69; Conservative

QY 1 NLVQFGVMIEKMTGK-SALQYNDYGCYGGIGSHWPDQTDWCCHADCCYGRLEKLGCE 59
 Db 21 NLVNFHRIKLTGTGEAALSFGYCHGVGRSGPKDATDCCVTHDCCYKLEKRGCG 80

QY 60 PKLEKYLFSVSRGIFCAGRTTCORLTCECDKRAALCFRNLTGYNRYAHYPNKLTGP 119
 Db 81 TKFLSYKFSNLSGRITCAKQDSCRSQLCEDKAAATCFARNKTTYNKYQYYSNKHCRGS 140

QY 120 TPQC 123
 Db 141 TPRC 144

RESULT 3

S13019
 Phospholipase A2 (EC 3.1.1.4) - horn viper
 C;Species: Cerastes cerastes (horn viper)
 C;Date: 19-Mar-1997 #sequence revision 19-Mar-1997 #text_change 31-Oct-1997
 C;Accession: S13019
 R;Siddiqi, A.R.; Shafiqat, J.; Zaidi, Z.H.; Joernvall, H.
 FEBS Lett. 278, 14-16, 1991
 A;Title: Characterization of phospholipase A2 from the venom of Horned viper (Cerastes ca
 A;Reference number: S13019; MUID:91130587; PMID:1993470
 A;Accession: S13019
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-120 <SID>
 C;Superfamily: phospholipase A2
 C;Keywords: carboxylic ester hydrolase

Query Match 49.7%; Score 358.5; DB 2; Length 120;
 Best Local Similarity 54.2%; Pred. No. 1e-27;
 Matches 64; Conservative 10; Mismatches 41; Indels 3; Gaps 2;

QY 1 NLVQFGVMIEKMTGKSAI-QYNDYGCYGGIGSHWPDQTDWCCHADCCYGRLEKLGCE 59
 Db 1 NLVQFGVMIFKMTGKSPFISYGDYGCYCGWGKGTPVDATDRCDFVHDCCYGRVN--SCN 58

QY 60 PKLEKYLFSVSRGIFCAGRTTCORLTCECDKRAALCFRNLTGYNRYAHYPNKLTCT 117
 Db 59 PKRSTYSYFQNGIVGDDQNLCKRAVCECDRAAICFGENVNTYDKYKDYPTSQCT 116

RESULT 4

S22388
 phospholipase A2 (EC 3.1.1.4) amodytin I2 precursor - western sand viper
 C;Species: Vipera ammodytes ammodytes (western sand viper)

Db 1 NLFQFEKLKQVTKSGMLWYSAYGVCYGGQGRPKDADTRCQFVHDCYGVK--TGCN 58

Qy 60 PLEKYLFSVSRGIFCAGRITTCORLTCECDKRAALCFRNLTGYNKK-YAHYPNKLCTG 118
 |: : : |: : : |: : : |: : : |: : : |: : : |: : : |: : : |: : : |: : :
 Db 59 PWDIVTYSVDNGNIVCGGTNPCKKQICECDRAAICFRDNLKTYDSKTWKYPKNCKE 118
 |: : : |: : : |: : : |: : : |: : : |: : : |: : : |: : : |: : : |: : :
 Qy 119 PTPPC 123
 : : :
 Db 119 ESEPC 123
 : : :
 RESULT 6
 A33394
 phospholipase A2 (EC 3.1.1.4) precursor (version 1) - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 20-Jun-2000
 C/Accession: A33394; J00131
 R/Ichizaki, J.; Ohara, O.; Nakamura, E.; Tanaki, M.; Ono, T.; Kanda, A.; Yoshii, B.
 Biochem. Biophys. Res. Commun. 162, 1030-1036, 1989
 A/Title: cDNA cloning and sequence determination of rat membrane-associated phospholipase A2
 A/Reference number: A33394; MUID:89350908; PMID:2764915
 A/Accession: A33394
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Molecule type: mRNA
 A/Residues: 1-146 <ISH>
 A/Cross-references: GB:M25148
 R/Komada, M.; Kudo, I.; Mizushima, H.; Kitamura, N.; Inoue, K.
 J. Biochem. 106, 545-547, 1989
 A/Title: Structure of cDNA coding for rat platelet phospholipase A2.
 A/Reference number: J00131; MUID:90110043; PMID:2606907
 A/Accession: J00131
 A/Molecule type: mRNA
 A/Residues: 1-146 <KOM>
 A/Cross-references: GB:D00523; NID:g220857; PIDN:BAA00410.1; PID:g220858
 C/Superfamily: phospholipase A2
 C/Keywords: carboxylic ester hydrolase
 F/1-21/Domain: signal sequence #status predicted <SIG>
 F/22-146/Product: phospholipase A2 #status predicted <MAT>
 F/69,113/Active site: His, Asp #status predicted

Query Match 48.1%; Score 347; DB 2; Length 146;
 Best Local Similarity 51.2%; Pred. No. 1.6e-25;
 Matches 64; Conservative 14; Mismatches 45; Indels 2; Gaps 2

Qy 1 NLVQFGWTEKMTGKSA-LQYNDYGCYCGGSHWPVDQDWCHAHDCCYGRLEKLGC 59
 :
 Db 22 SLLEFGQMLFXTGRADYSYFGYCHGCVGRGSPKDATDWCVTHTDCCVNFLEKRGCG 81
 :
 Qy 60 PLEKYLFSVSRGIFCA-GRITTCORLTCECDKRAALCFRNLTGYNKKYAHYPNKLCTG 118
 |: : : |: : : |: : : |: : : |: : : |: : : |: : : |: : : |: : : |: : : |: : : |: : :
 Db 82 TKFLTYKFSYRGQGQISCTNQDSCKRQLQCDDKAAACEFARNKKSYSLKYPFNKFCRG 141
 :
 Qy 119 PTPPC 123
 : : :
 Db 142 KTFSC 146
 : : :
 RESULT 7
 PSBGAC
 phospholipase A2 (EC 3.1.1.4) - horned viper
 N/Alternate names: caudoxin; phosphatidylcholine 2-acylhydrolase
 C/Species: Bitis caudalis (horned viper)
 C/Date: 17-Dec-1992 #sequence_revision 17-Dec-1992 #text_change 24-Apr-1998
 C/Accession: A00762
 R/Viljoen, C.C.; Botes, D.P.; Kruger, H.
 Toxicon 20, 715-737, 1982
 A/Title: Isolation and amino acid sequence of caudoxin, a presynaptic acting toxin
 A/Reference number: A00762; MUID:83042262; PMID:7135414
 A/Accession: A00762
 A/Molecule type: protein
 A/Residues: 1-121 <VIL>
 C/Comment: This enzyme is a presynaptic neurotoxin.
 C/Function:

A;Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-acyl-
A;Note: the reaction is strongly enhanced when the phospholipid is condensed into a micelle
C;Superfamily: phospholipase A2
C;Keywords: calcium; carboxylic ester hydrolase; lipid degradation; metalloprotein; pres
F;25-121,27-43,42-94,48-114,49-87,56-80,74-85/Disulfide bonds: #status predicted
F;26,28,30,47/Binding site: calcium (Tyr, Gly, Asp) #status predicted
F;46,88/Active site: His, Asp #status predicted

Query Match 47.1%; Score 340; DB 1; Length 121;
Best Local Similarity 47.2%; Pred. No. 6.3e-26;
Matches 58; Conservative 15; Mismatches 48; Indels 2; Gaps 1;
QY 1 NLVQFGVMEIKWTGKSA-LQYNDYCYGCGIGGSHWVPDQTDWCCHADCCYGRLEKLGCEP 60
DB 1 NLIQFGNMISATYKSSLAYASYGCGYGGGKQGFQDDTRCCFVHDCCYEKL--TGCD 58
QY 61 KLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRYAHYPNKLTCTGPT 120
DB 59 KMILSYKFNHNGNIVCGDKNAKKKVCEDRVAICFAASGHYNNKLYWYPSKCTGTA 118
QY 121 PPC 123
DB 119 EKC 121

RESULT 8

PSVXF
phospholipase A2 (EC 3.1.1.4) X - habu
N;Alternate names: phosphatidylcholine 2-acylhydrolase
C;Species: Trimeresurus flavoviridis (habu)
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 24-Apr-1998
C;Accession: A25500
R;Kinii, R.M.; Kawabata, S.I.; Iwanaga, S.
Toxicon 24, 1117-1129, 1986
A;Title: Comparison of amino terminal region of three isoenzymes of phospholipases A2 (T
A;Note: the reaction is strongly enhanced when the phospholipid is condensed into a micelle
C;Superfamily: phospholipase A2
C;Keywords: calcium; carboxylic ester hydrolase; homodimer; lipid degradation; metallopro
F;26-122,28-44,43-95,49-115,50-88,57-81,75-86/Disulfide bonds: #status predicted
F;27,29,31,48/Binding site: calcium (Tyr, Gly, Asp) #status predicted
F;47,89/Active site: His, Asp #status predicted

Query Match 47.0%; Score 339.5; DB 1; Length 122;
Best Local Similarity 49.2%; Pred. No. 7.1e-26;
Matches 61; Conservative 16; Mismatches 44; Indels 3; Gaps 2;

QY 1 NLVQFGVMEIKWTGKSA-LQYNDYCYGCGIGGSHWVPDQTDWCCHADCCYGRLEKLGCE 59
DB 1 HLLQFRMKIKMTGKEPIVSFAFYCYGCGGGRGKPKDADTRCCFVHDCCYEKL--TGCD 58
QY 60 PKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRYAHYPNKLTCTGP 119
DB 59 PKWSYTYTSLNGDIVCGDPVCTKVKCECDKAAICFRDNLKTYKNRYMTFPDICTDP 118

QY 120 TPPC 123

DB 119 TEGC 122

RESULT 9

JC1342
phospholipase A2 (EC 3.1.1.4) precursor - halys viper
C;Species: Agkistrodon halys (halys viper)
C;Date: 09-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 13-Nov-1998
C;Accession: JG1342
R;Pan, H.; Ou-Yang, L.L.; Yang, G.Z.; Zhou, Y.C.; Wu, X.F.

Acta Biochim. Biophys. Sin. 28, 579-582, 1996

A;Title: Cloning of the BPLA2 Gene from Agkistrodon halys Pallas.

A;Reference number: JG1342

A;Contents: Snake venom

A;Accession: JG1342

A;Molecule type: mRNA

A;Residues: 1-138 <PAN>

A;Note: the authors translated the codon GAC for residue 54 as Asn

C;Comment: This protein catalyzes specifically the hydrolysis of the C-2 ester bond of 3-

C;Superfamily: phospholipase A2

C;Keywords: carboxylic ester hydrolase

F;1-16/Domain: signal sequence #status predicted <SIG>

F;17-138/Product: phospholipase A2 #status predicted <MAT>

Query Match 47.0%; Score 339.5; DB 2; Length 138;
Best Local Similarity 50.0%; Pred. No. 7.9e-26;
Matches 62; Conservative 15; Mismatches 44; Indels 3; Gaps 2;

QY 1 NLVQFGVMEIKWTGKS-ALQYNDYCYGCGIGGSHWVPDQTDWCCHADCCYGRLEKLGCE 59

DB 17 SLLQFRMKIKMTGKEPIVSFAFYCYGCGGGRGKPKDADTRCCFVHDCCYEKL--TGCD 74

QY 60 PKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRYAHYPNKLTCTGP 119

DB 75 PKWDDYTYSWKNGTIVCGDDPCKEVECECDKAAICFRDNLKTYKNRYMTYPNLCSSK 134

QY 120 TPPC 123

DB 135 SEKC 138

RESULT 10

A35493

phospholipase A2 (EC 3.1.1.4) II precursor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 14-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 18-Jun-1999

C;Accession: A35493; S11388; S71310

R;Komada, M.; Kudo, I.; Inoue, K.

Biochem. Biophys. Res. Commun. 168, 1059-1065, 1990

A;Title: Structure of gene coding for rat group II phospholipase A-2.

A;Reference number: A35493; MUID:90267443; PMID:2346480

A;Accession: A35493

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-146 <KOM>

A;Cross-references: GB:M37127; NID:G204318; PIDN:AAA41223.1; PID:G204319

A;Note: the authors translated the codon TAT for residue 42 as Thr

R;Kusunoki, C.; Satoh, S.; Kobayashi, M.; Niwa, M.

Biochim. Biophys. Acta 1087, 95-97, 1990

A;Title: Structure of genomic DNA for rat platelet phospholipase A(2).

A;Reference number: S11388; MUID:90381322; PMID:2400792

A;Accession: S11388

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-146 <KUS>

A;Cross-references: EMBL:X51529; NID:G56930; PIDN:CAA35909.1; PID:G56931

R;Aarman, A.J.; Schalkwijk, C.G.; Neys, F.W.; Iijima, N.; Wherrett, J.R.; van den Bosch,

Arch. Biochem. Biophys. 331, 95-103, 1996

A;Title: Purification and characterization of Ca(2+)-dependent phospholipases A(2) from :

A;Reference number: S71310; MUID:96268465; PMID:8660688

A;Accession: S71310

A;Molecule type: protein

A;Residues: 22-29, X'31-32, X'34 <AAR>

A;Experimental source: kidney

C;Superfamily: phospholipase A2

C;Keywords: carboxylic ester hydrolase; lipid degradation

F;68,113/Active site: His, Asp #status predicted

Query Match 46.7%; Score 337; DB 2; Length 146;

Best Local Similarity 50.4%; Pred. No. 1.4e-25;

Matches 63; Conservative 14; Mismatches 46; Indels 2; Gaps 2;

QY 1 NLVQFGVMEIKWTGKSA-LQYNDYCYGCGIGGSHWVPDQTDWCCHADCCYGRLEKLGCE 59

Db 22 SLLEFGQMIILFKTKRADVSYGFVGCCHGVGGGRSPKDATDWCCVTHDCCYNLEKRGCG 81
Qy 60 PKLEKYLFSVSERGIFCA-GRTTTCORLTCECDKRAALCFERNLGTNYARKYAHYPNKLCTG 118
Db 82 TKFLTYKFSYRGQGISCTWODSCRKQLCCQDKRAAECFARNKKSYSLSKYQFYLNKFCKG 141
Qy 119 PTPPC 123
Db 142 KTPSC 146
RESULT 11
I50098
Phospholipase a2 - jararacussu
C/Species: Bothrops jararacussu (jararacussu)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 18-Jun-1999
C/Accession: I50098; S44247
R/Moura-da-Silva, A.M.; Paine, M.J.; Diniz, M.R.; Theakston, R.D.; Crampton, J.M.
J. Mol. Evol. 41, 174-179, 1995
A/Title: The molecular cloning of a phospholipase A2 from Bothrops jararacussu snake venom
A/Reference number: I50098; MUID:95395872; PMID:7666446
A/Accession: I50098
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-138 <MOU>
A/Cross-references: EMBL:X76289; NID:g475923; PIDN:CAA53921.1; PID:g475924
C/Genetics:
A/Gene: PLA-2
C/Suprafamily: phospholipase A2
F/63,105/Active site: His, Asp #status predicted
Query Match 46.5%; Score 335.5; DB 2; Length 138;
Best Local Similarity 50.0%; Pred. No. 1.9e-25;
Matches 62; Conservative 12; Mismatches 47; Indels 3; Gaps 2;
Qy 1 NLVQFGWMIKMTGKSL-QYNDYGCYCGIGGSHWPVDQTDWCHAHDCYGRLEKLGCE 59
Db 17 DLWQFGQMIILKTKLPFPFYTTYGYCGWGGQGPXDATDRCCFVHDCYCKL--TNCK 74
Qy 60 PKLEKYLFSVSERGIFCAGRTTCORLTCECDKRAALCFERNLGTNYARKYAHYPNKLCTGP 119
Db 75 PKYDRYSRENGVITCEGTPECKICECDKRAAAVCFERNLTYKRYNAYPDVLCCKP 134
Qy 120 TTPC 123
Db 135 AEKC 138
RESULT 12
I48342
Phospholipase A2 (EC 3.1.1.4), secretory group II - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
C/Accession: I48342; PC2009; S35948; I49352
R/Mulherkar, R.; Rao, R.S.; Wagle, A.S.; Patki, V.; Deo, M.G.
Biochem. Biophys. Res. Commun. 197, 1254-1263, 1993
A/Title: Enhancing factor, a Paneth cell specific protein from mouse small intestines:
A/Reference number: I48342; MUID:94029955; PMID:8267767
A/Accession: I48342
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-146 <NULL>
A/Cross-references: EMBL:X74266; NID:g557247; PIDN:CAA52325.1; PID:g557248
R/Mulherkar, R.; Rao, R.S.; Wagle, A.S.; Patki, V.; Deo, M.G.
Biochem. Biophys. Res. Commun. 197, 351-352, 1993
A/Title: Enhancing factor, a paneth cell specific protein from mouse small intestines:
A/Reference number: PC2009; MUID:94071967; PMID:8250944
A/Accession: PC2009
A/Molecule type: mRNA
A/Residues: 22-146 <MUL2>
A/Note: correction of S35948
R/Mulherkar, R.; Rao, R.; Wagle, A.; Patki, V.; Deo, M.

S10333
ammodytoxin B precursor - sand viper
C:Species: Vipera ammodytes (sand viper)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999
C:Accession: S10333
R:Kordis, D.; Pungercar, J.; Strukelj, B.; Liang, N.; Gubensek, F.
Nucleic Acids Res. 18, 4016, 1990
A:Title: Sequence of the cDNA coding for ammodytoxin B.
A:Reference number: S10333; MUID:90326552; PMID:2374735
A:Accession: S10333
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-138 <KOR>
A:Cross-references: EMBL:X52241; NID:964441; PIDN:CAA36486.1; PID:964442
C:Superfamily: phospholipase A2

Query Match 46.2%; Score 333.5; DB 2; Length 138;
Best_Local_Similarity 47.6%; Pred.No.3e-25; 44; Indels 3; Gaps 2;
Matches 59; Conservative 18; Mismatches 44;
Qy 1 NLVQGVMIKMTGKSA-LQYNDYGCYGGSHWPVDQTDWCHAHDCCYGRLEKLGCE 59
Db 17 SLLEFGMILGETGKNPLTSYFYGCYGVGKGTDXDTRCFVHDCCYGNLP--DCS 74
Qy 60 PKLEKYLFSVSRGIFCA-GRITTCQRLTCECDKRAALCFRNLGTYNRYAHYENKLTGP 119
Db 75 PKTRYKHYRNGAIVCGKGTSCNRCICEDRAAAICFRKNLKTYNHYMYTFDLCKE 134
Qy 120 TPPC 123
Db 135 SEKC 138

RESULT 15
JU0283
phospholipase A2 (EC 3.1.1.4) precursor (version 2) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 24-Jul-1997
C:Accession: JU0283
R:Komada, M.; Kudo, I.; Mizushima, H.; Kitamura, N.; Inoue, K.
J. Biochem. 106, 545-547, 1989
A:Title: Structure of cDNA coding for rat platelet phospholipase A2.
A:Reference number: JU0131; MUID:90110043; PMID:2606907
A:Accession: JU0283
A:Molecule type: mRNA
A:Residues: 1-146 <KOM>
C:Superfamily: phospholipase A2
C:Keywords: carboxylic ester hydrolase
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-146/Product: phospholipase A2 #status predicted <MAT>
F:68,113/Active site: His, Asp #status predicted

Query Match 46.1%; Score 333; DB 2; Length 146;
Best_Local_Similarity 49.6%; Pred.No.3.5e-25; 47; Indels 2; Gaps 2;
Matches 62; Conservative 14; Mismatches 47;
Qy 1 NLVQGVMIKMTGKSA-LQYNDYGCYGGSHWPVDQTDWCHAHDCCYGRLEKLGCE 59
Db 22 SLLEFGQMILFKTRADVSYFYGCYGVGGRSPKDATDWCCTHGCCYNLLEKRGCG 81
Qy 60 PKLEKYLFSVSRGIFCA-GRITTCQRLTCECDKRAALCFRNLGTYNRYAHYENKLTGP 118
Db 82 TKFLTYSYRGGGQISCSSTNODSCRKQLCCDKAAABCFARNKKSYSLKTYQYFNPFCG 141
Qy 119 TPPC 123
Db 142 KTPSC 146

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 3, 2004, 05:12:38 ; Search time 8.81897 Seconds
(without alignments)
726.242 Million cell updates/sec

Title: US-10-088-092a-30_COPY_20_142
Perfect score: 722
Sequence: 1 NLVQFGVMIKMTGKSALQY.....YNEKYAHYPNKLTGTPPC 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	722	100.0	142	1 PA2E HUMAN	Q9nzk7 homo sapien
2	662	91.7	142	1 PA2E MOUSE	Q9nzk3 mus musculus
3	372	51.5	121	1 PA21 ERIMA	P24393 eristocophi
4	360.5	49.9	144	1 PA21 HUMAN	P14555 homo sapien
5	358.5	49.7	120	1 PA2 CERCE	P21789 cerastes ce
6	358	49.6	137	1 PA2N VIPAA	P34180 vipera ammo
7	355	49.2	121	1 PA2 DABRR	P81458 daboia russ
8	350	48.5	123	1 PA21 AGKPI	P51972 agkistrodon
9	347	48.1	146	1 PA2A RAT	P14423 rattus norv
10	344.5	47.7	138	1 PA2Q TRIFL	Q8j190 trimeresuru
11	344.5	47.7	138	1 PA2Y TRIFL	Q90y77 trimeresuru
12	341	47.2	146	1 PA2A MOUSE	P31482 mus musculus
13	340.5	47.2	122	1 PA2A TRIFL	P59264 trimeresuru
14	340	47.1	121	1 PA2 BITCA	P00622 bitis cauda
15	339.5	47.0	122	1 PA2X TRIFL	P06860 trimeresuru
16	339.5	47.0	138	1 PA2A AGKHP	Q42187 agkistrodon
17	339	47.0	137	1 PA2B VIPPA	Q9y9j7 vipera pala
18	338.5	46.9	122	1 PA29 AGKHP	P42188 agkistrodon
19	338.5	46.9	122	1 PA2B TRIFL	P59265 trimeresuru
20	337.5	46.7	138	1 PA2W TRIFL	Q02517 trimeresuru
21	335.5	46.5	138	1 PA21 BOTJR	P45881 bothrops ja
22	334.5	46.3	138	1 PA2B TRIGA	P70088 trimeresuru
23	333.5	46.2	138	1 PA2B VIPAA	P14424 vipera ammo
24	332.5	46.1	141	1 PA2B DABRR	P59071 daboia russ
25	332.5	46.1	122	1 PA22 AGKHA	P20249 agkistrodon
26	332.5	46.1	122	1 PA2 VIPBB	P31854 vipera beru
27	330.5	45.8	138	1 PA2A VIPAA	P11407 vipera ammo
28	330.5	45.8	138	1 PA2C VIPAA	P10427 vipera ammo
29	329.5	45.6	122	1 PA22 TRIGA	P81478 trimeresuru
30	328.5	45.5	122	1 PA21 AGKHA	P04417 agkistrodon
31	327.5	45.4	138	1 PA2 TRIGU	Q8j1y9 trimeresuru
32	326.5	45.2	138	1 PA22 TRIMU	Q91968 trimeresuru
33	326.5	45.2	138	1 PA2A TRIMU	Q90w39 trimeresuru

34	325.5	45.1	121	1 PA22 ERIMA	P24294 eristocophi
35	325.5	45.1	122	1 PA28 AGKHP	Q42192 agkistrodon
36	325.5	45.1	138	1 PA2P TRIFL	Q92147 trimeresuru
37	324.5	44.9	122	1 PA23 TRIGA	P81480 trimeresuru
38	324.5	44.9	138	1 PA25 ECHOC	P59171 echis ocell
39	324	44.9	124	1 PA26 AGKHP	O42190 agkistrodon
40	324	44.9	145	1 PA2M CAVPO	P47711 cavia porce
41	321.5	44.5	122	1 PA23 AGKHP	P14421 agkistrodon
42	320.5	44.4	122	1 PA21 TRIMU	Q91506 trimeresuru
43	319.5	44.3	138	1 PA21 TRIGA	P20476 trimeresuru
44	319.5	44.3	138	1 PA2A CROSS	P18998 crotalus sc
45	318.5	44.1	122	1 PA21 BOTAS	P20474 bothrops as

ALIGNMENTS

RESULT 1	PA2E HUMAN	STANDARD;	PRT;	142 AA.
ID	Q9NZK7			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Group IIE secretory phospholipase A2 precursor (EC 3.1.1.4)			
DE	(Phosphatidylcholine 2-acylhydrolase GIIE) (GIIE SPLA2) (SPLA(2)-IIE).			
GN	PLA2G2E.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND CHARACTERIZATION.			
RX	MEDLINE=20148788; PubMed=10681567;			
RA	Suzuki N., Ishizaki J., Yokota Y., Higashino K., Ono T., Ikeda M.,			
RA	Fujii N., Kawamoto K., Hanasaki K.;			
RT	"Structures, enzymatic properties, and expression of novel human and			
RT	mouse secretory phospholipase A(2)s.";			
RL	J. Biol. Chem. 275:5785-5793(2000).			
CC	!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-			
CC	acyl groups in 3-sn-phosphoglycerides. Has a preference for			
CC	arachidonic-containing phospholipids.			
CC	!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-			
CC	acylglycerophosphocholine + a fatty acid anion.			
CC	!- COFACTOR: Binds 1 calcium ion per subunit.			
CC	!- SUBCELLULAR LOCATION: Secreted.			
CC	!- TISSUE SPECIFICITY: Restricted to the brain, heart, lung, and			
CC	placenta.			
CC	!- SIMILARITY: Belongs to the phospholipase A2 family.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL; AF189279; AAF36541.1; -.			
CC	HSSP; P14555; 1POD.			
DR	GO; GO:0004624; F:secreted phospholipase A2 activity; TAS.			
DR	GO; GO:0006954; P:inflammatory response; TAS.			
DR	GO; GO:0006644; P:phospholipid metabolism; TAS.			
DR	InterPro; IPR001211; PhospholipaseA2.			
DR	Fam; PF00068; Phoslip; 1.			
DR	PRINTS; PR00389; PHPLIPASEA2.			
DR	ProDom; PD000303; PhospholipaseA2; 1.			
DR	SMART; SM00085; PA2c; 1.			
DR	PROSITE; PS00119; PA2_ASP; FALSE_NEG.			
DR	PROSITE; PS00118; PA2_HIS; 1.			
KW	Hydrolase; Lipid degradation; Signal; Calcium.			
FT	SIGNAL 1 19 POTENTIAL.			
FT	CHAIN 20 142 GROUP IIE SECRETORY PHOSPHOLIPASE A2.			

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FT ACT SITE 65 65 BY SIMILARITY.
FT ACT SITE 109 109 BY SIMILARITY.
FT DISULFID 44 135 BY SIMILARITY.
FT DISULFID 46 62 BY SIMILARITY.
FT DISULFID 61 115 BY SIMILARITY.
FT DISULFID 67 142 BY SIMILARITY.
FT DISULFID 68 108 BY SIMILARITY.
FT DISULFID 77 101 BY SIMILARITY.
FT DISULFID 95 106 BY SIMILARITY.
FT METAL 45 45 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 47 47 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 49 49 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 66 66 CALCIUM (BY SIMILARITY).
SQ SEQUENCE 142 AA; 15989 MW; 3C360EA710E141FB CRC64;

Query Match 100.0%; Score 722; DB 1; Length 142;
Best Local Similarity 100.0%; Pred. No. 5.4e-71; Indels 0; Gaps 0;
Matches 123; Conservative 0; Mismatches 0;

QY 1 NLVQGVGMIEKMTGKSAQYNDYCYCGIGGSHWPFVDQTCWCHAHDCCYGRLEKLGCEP 60
DB 20 NLVQGVGMIEKMTGKSAQYNDYCYCGIGGSHWPFVDQTCWCHAHDCCYGRLEKLGCEP 79
QY 61 KLEKYLFSVSEGIKAGRTTCORLTCECDKRAALCFRNLTGNRYKVAHYPNKLTGTPT 120
DB 80 KLEKYLFSVSEGIKAGRTTCORLTCECDKRAALCFRNLTGNRYKVAHYPNKLTGTPT 139
QY 121 PPC 123
DB 140 PPC 142

RESULT 2
PAZE MOUSE
ID PAZE MOUSE STANDARD; PRT; 142 AA.
AC Q9QUL3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Group IIE secretory phospholipase A2 precursor (EC 3.1.1.4)
DE (Phosphatidylcholine 2-acylhydrolase G1IE) (G1IE sPLA2) (sPLA(2)-IIE).
GN PLA2G2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20002639; PubMed=10531313;
RA Valentin E., Ghomashchi F., Gelb M.H., Lazdunski M., Lambeau G.;
RT "On the diversity of secreted phospholipases A2. Cloning, tissue
RT distribution, and functional expression of two novel mouse group II
RT enzymes."
RL J. Biol. Chem. 274:31195-31202(1999).
RN [2]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=BALB/c;
RA Suzuki N., Ishizaki J., Yokota Y., Higashino K., Ono T., Ikeda M.,
RA Fujii N., Kawamoto K., Hanasaki K.;
RT "Structures, enzymatic properties, and expression of novel human and
RT mouse secretory phospholipase A(2)s."
RL J. Biol. Chem. 275:5785-5793(2000).
CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
CC acyl groups in 3-sn-phosphoglycerides.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a fatty acid anion.
CC -!- COFACTOR: Binds 1 calcium ion per subunit.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Highly expressed in uterus, and at lower

```

```

CC levels in various other tissues.
CC -!- SIMILARITY: Belongs to the phospholipase A2 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF166098; AAF04499.1; -.
CC DR EMBL; AF112984; AAF22290.1; -.
CC DR HSSP; P14555; 1POD.
CC DR MGD; MGI:1349660; Pla2g2a.
CC DR InterPro; IPR001211; PhospholipaseA2.
CC DR Pfam; PF00068; phoslip; 1.
CC DR PRINTS; PRO0389; PHPLIPASEA2.
CC DR ProDom; PD000303; PhospholipaseA2; 1.
CC DR SMART; SM00085; PA2c; 1.
CC DR PROSITE; PS00119; PA2 ASP; FALSE_NEG.
CC DR PROSITE; PS00118; PA2_HIS; 1.
CC DR HydroLase; Lipid degradation; Signal; Calcium.
KW SIGNAL 1 19
FT CHAIN 20 142 GROUP IIE SECRETORY PHOSPHOLIPASE A2.
FT ACT SITE 65 65 BY SIMILARITY.
FT ACT SITE 109 109 BY SIMILARITY.
FT DISULFID 44 135 BY SIMILARITY.
FT DISULFID 46 62 BY SIMILARITY.
FT DISULFID 61 115 BY SIMILARITY.
FT DISULFID 67 142 BY SIMILARITY.
FT DISULFID 68 108 BY SIMILARITY.
FT DISULFID 77 101 BY SIMILARITY.
FT DISULFID 95 106 BY SIMILARITY.
FT METAL 45 45 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 47 47 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 49 49 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 66 66 CALCIUM (BY SIMILARITY).
SQ SEQUENCE 142 AA; 15942 MW; 8B0E3CC710A1F946 CRC64;

Query Match 91.7%; Score 662; DB 1; Length 142;
Best Local Similarity 88.6%; Pred. No. 1.6e-64;
Matches 109; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 NLVQGVGMIEKMTGKSAQYNDYCYCGIGGSHWPFVDQTCWCHAHDCCYGRLEKLGCEP 60
DB 20 NLVQGVGMIEKMTGKSAQYNDYCYCGIGGSHWPFVDQTCWCHAHDCCYGRLEKLGCEP 79
QY 61 KLEKYLFSVSEGIKAGRTTCORLTCECDKRAALCFRNLTGNRYKVAHYPNKLTGTPT 120
DB 80 KLEKYLFSITRDNIFCAGRTACQRTCECDKRAALCFRNLTGNRYKVAHYPNKLTGTPT 139
QY 121 PPC 123
DB 140 PPC 142

RESULT 3
PA21 ERIMA
ID PA21 ERIMA STANDARD; PRT; 121 AA.
AC P24293;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Phospholipase A2 isozyme PLA-1 (EC 3.1.1.4) (Phosphatidylcholine
DE 2-acylhydrolase).
OS Eristocophis macmahoni (leaf-nosed viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Eristocophis.

```

OX NCBI_TaxID=8702;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=92037623; PubMed=1935962;
RA Siddiqi A.R., Zaidi Z.H., Joernvall H.;
RT "Purification and characterization of two highly different group II
RT phospholipase A2 isozymes from a single viperid (Eristocophis
RT macmahoni) venom.";
RL Eur. J. Biochem. 201;675-679 (1991).
CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
CC acyl groups in 3-sn-phosphoglycerides.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a fatty acid anion.
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the phospholipase A2 family. Group II
CC subfamily.
DR PR; S17860; S17860.
DR HSP; P81458; 1VIP.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; Phoslip; 1.
DR PRINTS; PR00389; PHPLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2c; 1.
DR PROSITE; PS00119; PA2_ASP; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
KW Hydrolase; Lipid degradation; Calcium; Multigene family.
FT ACT_SITE 47 47
FT ACT_SITE 89 89
FT ACT_SITE 115 115
FT DISULFID 28 44
FT DISULFID 43 95
FT DISULFID 49 121
FT DISULFID 50 88
FT DISULFID 57 81
FT DISULFID 75 86
FT METAL 27 27
FT METAL 29 29
FT METAL 31 31
FT METAL 48 48
SQ SEQUENCE 121 AA; 13533 MW; F5BA64676954B5E CRC64;
Query Match 51.5%; Score 372; DB 1; Length 121;
Best Local Similarity 56.5%; Pred. No. 2.8e-33;
Matches 70; Conservative 8; Mismatches 42; Indels 4; Gaps 3;
Qy 1 NLVQFGVWIEKMTGKSA-LOYNDYGCYGGIGGSHWPVDQTDWCHADCCYGLEKLGCE 59
Db 1 NLVQFGKVI FMTYKSAALLSYDYGCGYGGKGLPDAIDRCFVHDCCYGRVN--GCN 58
Qy 60 PKLEKLYFSVSEIRGIFCAGRTTCQRLTCECDKKAALCFRRNLGTYNRKYAHYPNKLCITGP 119
Db 59 PKLSTYSYFQNGDIVCGDDNACLRAVCECDRAAICFGENLNTYDRKKYDPSQCT-E 117
Qy 120 TPPC 123
Db 118 TEQC 121
RESULT 4
PA2A_HUMAN STANDARD; PRT; 144 AA.
AC P14555; Q9UCD2;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Phospholipase A2, membrane associated precursor (EC 3.1.1.4)
DE (Phosphatidylcholine 2-acylhydrolase) (Group IIA phospholipase A2)
DE (GIIC sPLA2) (Non-pancreatic secretory phospholipase A2) (NPS-PLA2).

GN PLA2G2A OR PLA2B OR RASP-A OR PLA2L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Rheumatoid arthritic synovial fluid;
RX MEDLINE=89174566; PubMed=2925608;
RA Seihamer J.J., Pruzanski W., Vadas P., Plant S., Miller J.A.,
RA Kloss J., Johnson L.K.;
RT "Cloning and recombinant expression of phospholipase A2 present in
RT rheumatoid arthritic synovial fluid.";
RL J. Biol. Chem. 264:5335-5338 (1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89174633; PubMed=2925633;
RA Kramer R.M., Hession C., Johansen B., Hayes G., McGray P., Chow E.P.,
RA Tizard R., Pepinsky R.B.;
RT "Structure and properties of a human non-pancreatic phospholipase
RT A2.";
RL J. Biol. Chem. 264:5768-5775 (1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=91050834; PubMed=2239446;
RA Kramer R.M., Johansen B., Hession C., Pepinsky R.B.;
RT "Structure and properties of a secreted phospholipase A2 from human
RT platelets.";
RL Adv. Exp. Med. Biol. 275:35-53 (1990).
RN [4]
RP SEQUENCE FROM N.A.
RX TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Toshiki S., Carninci P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [5]
RP SEQUENCE OF 21-144.
RC TISSUE=Spleen;
RX MEDLINE=89374261; PubMed=2775276;
RA Kanda A., Ono T., Yoshida N., Tojo H., Okamoto M.;
RT "The primary structure of a membrane-associated phospholipase A2 from
RT human spleen.";
RL Biochem. Biophys. Res. Commun. 163:42-48 (1989).
RN [6]
RP SEQUENCE OF 21-54.
RC TISSUE=Synovial fluid;
RX MEDLINE=89197814; PubMed=3240982;
RA Hara S., Kudo I., Matsuta K., Miyamoto T., Inoue K.;
RT "Amino acid composition and NH2-terminal amino acid sequence of human
RT phospholipase A2 purified from rheumatoid synovial fluid.";
RL J. Biochem. 104:326-328 (1988).
RN [7]
RP SEQUENCE OF 21-33.
RC TISSUE=Synovial fluid;
RX MEDLINE=89076274; PubMed=3202859;

RA Lai C.Y., Wada K.;
RT "Phospholipase A2 from human synovial fluid: purification and
RT structural homology to the placental enzyme.";
RL Biochem. Biophys. Res. Commun. 157:488-493(1988).
RN (8)
RP SEQUENCE OF 21-75.
RC TISSUE=ileal mucosa;
RX MEDLINE=94002200; PubMed=8399335;
RA Minami T., Tojo H., Shinomura Y., Matsuzawa Y., Okamoto M.;
RT "Purification and characterization of a phospholipase A2 from human
RT ileal mucosa";
RL Biochim. Biophys. Acta 1170:125-130(1993).
RN (9)
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=91287826; PubMed=20623281;
RA Wery J.-P., Schevitz R.W., Clawson D.K., Bobbitt J.L., Dow E.R.,
RT "Gambao G., Goodson T. Jr., Hermann R.B., McClure D.B.,
RA Mihelich E.D., Putnam J.E., Sharp J.D., Stark D.H., Teater C.,
RA Warrick M.W., Jones N.D.;
RT "Structure of recombinant human rheumatoid arthritic synovial fluid
RT phospholipase A2 at 2.2-A resolution.";
RL Nature 352:79-82(1991).
RN (10)
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=92054586; PubMed=1948070;
RA Scott D.L., White S.P., Browning J.L., Rosa J.J., Gelb M.H.,
RT "Structures of free and inhibited human secretory phospholipase A2
RT from inflammatory exudate.";
RL Science 254:1007-1010(1991).
RN (11)
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=93393225; PubMed=7664108;
RA Schreitz R.W., Bach N.J., Carlson D.G., Chirgadze N.Y., Clawson D.K.,
RA Dillard R.D., Draheim S.E., Hartley L.W., Jones N.D., Mihelich E.D.,
RA Olkowski J.L., Snyder D.W., Dand S.C., Wery J.-P.;
RT "Structure-based design of the first potent and selective inhibitor
RT of human non-pancreatic secretory phospholipase A2";
RL Nat. Struct. Biol. 2:458-465(1995).
RN (12)
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=96207049; PubMed=9538252;
RA Kitadokoro K., Hagishita S., Sato T., Ohtan M., Miki K.;
RT "Crystal structure of human secretory phospholipase A2-IIA complex
RT with the potent indolizine inhibitor 120-1032.";
RL J. Biochem. 123:619-623(1998).
CC -!- FUNCTION: Thought to participate in the regulation of the
CC phospholipid metabolism in biomembranes including eicosanoid
CC biosynthesis. Catalyzes the calcium-dependent hydrolysis of the 2-
CC acyl groups in 3-sn-phosphoglycerides.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a fatty acid anion.
CC -!- COFACTOR: Binds 1 calcium ion per subunit.
CC -!- SUBCELLULAR LOCATION: Membrane-associated.
CC -!- MISCELLANEOUS: Group II phospholipase A2 is found in many cells
CC and also extracellularly. The membrane-bound and secreted forms
CC are identical and are encoded by a single gene.
CC -!- SIMILARITY: Belongs to the phospholipase A2 family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M22430; AAA36550.1; -;
CC EMBL; M22431; AAA36549.1; -;
CC EMBL; BC005919; AAH05919.1; -;
CC PIR; A32862; PSUHYF.
CC PDB; 1AYP; 31-JUL-95.
CC PDB; 1BBC; 31-OCT-93.

DR PDB; 1POD; 31-OCT-93.
DR PDB; 1POE; 31-OCT-93.
DR PDB; 1KVO; 07-JUL-97.
DR PDB; 1DB4; 12-NOV-99.
DR PDB; 1DB5; 12-NOV-99.
DR PDB; 1DCY; 12-NOV-99.
DR Genew; HGNC:9031; FLA2G2A.
DR MIM; 172411; -;
DR GO; GO:0004623; F:phospholipase A2 activity; TAS.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PR00389; PHPLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PAZC; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
DR PROSITE; PS00119; PA2_ASP; 1.
KW Hydrolase; Lipid degradation; Membrane; Signal; Calcium;
KW 3D-structure.
FT SIGNAL 1 20
FT CHAIN 21 144
FT ACT_SITE 67 67
FT ACT_SITE 111 111
FT DISULFID 46 137
FT DISULFID 48 64
FT DISULFID 63 117
FT DISULFID 69 144
FT DISULFID 70 110
FT DISULFID 79 103
FT DISULFID 97 108
FT METAL 47 47
FT METAL 49 49
FT METAL 51 51
FT METAL 68 68
FT METAL 22 33
FT HELIX 37 40
FT TURN 41 41
FT TURN 45 47
FT HELIX 59 75
FT TURN 76 78
FT TURN 88 91
FT STRAND 92 93
FT STRAND 94 97
FT HELIX 102 120
FT TURN 121 121
FT TURN 122 124
FT TURN 127 128
FT TURN 127 128
Query Match 49.9%; Score 360.5; DB 1; Length 144;
Best Local Similarity 55.6%; Pred. No. 5.9e-32; Mismatches 45; Indels 1; Gaps 1;
Matches 69; Conservative 9;
QY 1 NLVQFQVMIKMTGK-SALQVNDYCYGICIGSHWPFVDQTDWCHAHDCCYGRLEKLGCE 59
Db 21 NLVNFHRIKLTGKEAALSFGYCHGCVGGRGSPKDATDRCCVTHDCCYKLEKRGCG 80
QY 60 PKLEYLFSVSRGIFPCAGRTTCQELTCECDKRALCFERNLGTNRKYAHVBNKLCCTGP 119
Db 81 TKFLSYKFSNGSRITCARQDSRQSCQLCECDRAAATCFARNKTYINKYQIYSNKHCRGS 140
QY 120 TPPC 123
Db 141 TPRC 144
RESULT 5
PA2 CERCE STANDARD; PRT; 120 AA.
ID PA2 CERCE
AC P21789;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Phospholipase A2 (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase).
OS Cerastes cerastes (Horned desert viper).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Viperinae; Cerastes.
 OX NCBI_TaxID=8697;
 RN [1]
 RN SEQUENCE.
 RP STRAIN=Baluchistan; TISSUE=Venom;
 RC MEDLINE=91130587; PubMed=1993470;
 RX Siddiqi A.R., Shafat J., Zaidi Z.H., Joernvall H.;
 RA "Characterization of phospholipase A2 from the venom of Horned viper
 RT (Cerastes cerastes).";
 RL FEBS Lett. 278:14-16 (1991).
 RN [2]
 RP SEQUENCE OF 1-31.
 RC STRAIN=Tunisia; TISSUE=Venom;
 RX MEDLINE=90385487; PubMed=2402760;
 RA Djebari F.L., Martin-Baucalire M.-F.;
 RT "Purification and characterization of a phospholipase A2 from
 RC Cerastes cerastes (horn viper) snake venom.";
 RL Toxicon 28:637-646 (1990).
 CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
 CC acyl groups in 3-sn-phosphoglycerides.
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a fatty acid anion.
 CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MISCELLANEOUS: Strains variations are extensive for this enzyme.
 CC -!- SIMILARITY: Belongs to the phospholipase A2 family. Group II
 CC subfamily.
 DR PIR; A35950; A35950.
 DR PIR; S13019; S13019.
 DR HSSP; P81458; 1VIP.
 DR - InterPro: IPR001211; PhospholipaseA2.
 DR Pfam; PF00068; Phoslip; 1.
 DR PRINTS; PR00389; PHPLIPASEA2.
 DR ProDom; PD000303; PhospholipaseA2; 1.
 DR SMART; SM00085; PA2c; 1.
 DR PROSITE; PS00119; PA2_ASP; 1.
 DR PROSITE; PS00118; PA2_HIS; 1.
 DR Hydrolase; Lipid degradation; Calcium.
 FT ACT_SITE 47 47
 FT ACT_SITE 89 89 BY SIMILARITY.
 FT ACT_SITE 26 115 BY SIMILARITY.
 FT DISULFID 28 44 BY SIMILARITY.
 FT DISULFID 43 95 BY SIMILARITY.
 FT DISULFID 50 88 BY SIMILARITY.
 FT DISULFID 57 81 BY SIMILARITY.
 FT DISULFID 75 86 BY SIMILARITY.
 FT METAL 27 27 CALCIUM (VIA CARBONYL OXYGEN)
 FT METAL 29 29 CALCIUM (VIA CARBONYL OXYGEN)
 FT METAL 31 31 CALCIUM (VIA CARBONYL OXYGEN)
 FT METAL 31 31 CALCIUM (VIA CARBONYL OXYGEN)
 FT METAL 48 48 CALCIUM (BY SIMILARITY).
 FT VARIANT 10 12 FRM -> KHK (IN STRAIN TUNISIA).
 FT VARIANT 17 19 PIF -> ALL (IN STRAIN TUNISIA).
 FT VARIANT -22 23 GD -> SA (IN STRAIN TUNISIA).
 SQ SEQUENCE 120 AA; 13534 MW; E6581FA7001C62C3 CRC64;
 Query Match 49.7%; Score 358.5; DB 1; Length 120;
 Best Local Similarity 54.2%; Pred. No. 8e-32;
 Matches 64; Conservative 10; Mismatches 41; Indels 3; Gaps 2;
 Qy 1 NLVQGVNIEKWTGKSL-QYNDYGCYGGHGWPDQDWCCHADCCYGRLEKLGCE 59
 Db 1 NLVQGVNIEKWTGKSL-QYNDYGCYGGHGWPDQDWCCHADCCYGRLEKLGCE 59
 Qy 60 PLEKYLFSVSEIRGIFCAGRTTORLTCECDKRAALCFRNLTGTNRYKHYHYNKLC 117
 Db 59 PKRSTYSYFQNGIIVCDQNLCKRAVCECDRAAICFGENVATYDKKYDYPTSOCT 116

RESULT 6
 ID PA2N VIPAA STANDARD; PRT; 137 AA.
 AC P34180; Q91967;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Phospholipase A2, neutral precursor (EC 3.1.1.4) (Ammodytin I2)
 DE (Phosphatidylcholine 2-acylhydrolase).
 GN AMI2.
 OS Vipera ammodytes ammodytes (Western sand viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Viperinae; Vipera.
 OX NCBI_TaxID=8705;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 17-137.
 RC TISSUE=Venom gland;
 RX MEDLINE=92201190; PubMed=1551386;
 RA Krizaj I., Liang N.-S., Pungercar J., Strukelj B., Ritonja A.,
 RA Gubensek F.;
 RT "Amino acid and cDNA sequences of a neutral phospholipase A2 from the
 RT long-nosed viper (Vipera ammodytes ammodytes) venom.";
 RL Eur. J. Biochem. 204:1057-1062 (1992).
 RN [2]
 RP REVISION TO 132.
 RA Pungercar J.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Kordis D., Gubensek F.;
 RT "Molecular evolution of phospholipase A2 multigene family in Vipera
 RT ammodytes.";
 RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
 CC acyl groups in 3-sn-phosphoglycerides.
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a fatty acid anion.
 CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the phospholipase A2 family. Group II
 CC subfamily.
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 CC -----
 CC EMBL; X56878; CAA40200.2; -.
 CC EMBL; X84018; CAA58840.1; -.
 CC PIR; S22388; S22388.
 CC HSSP; P81458; 1VIP.
 CC InterPro; IPR001211; PhospholipaseA2.
 CC Pfam; PF00068; Phoslip; 1.
 CC PRINTS; PR00389; PHPLIPASEA2.
 CC ProDom; PD000303; PhospholipaseA2; 1.
 CC SMART; SM00085; PA2c; 1.
 CC PROSITE; PS00119; PA2_ASP; 1.
 CC PROSITE; PS00118; PA2_HIS; 1.
 CC Hydrolase; Lipid degradation; Calcium; Signal;
 KW Multigene family.
 FT SIGNAL 1 16
 FT CHAIN 17 137 PHOSPHOLIPASE A2, NEUTRAL.
 FT ACT_SITE 63 63 BY SIMILARITY.
 FT ACT_SITE 105 105 BY SIMILARITY.
 FT DISULFID 42 131 BY SIMILARITY.
 FT DISULFID 44 60 BY SIMILARITY.
 FT DISULFID 59 111 BY SIMILARITY.
 FT DISULFID 65 137 BY SIMILARITY.
 FT DISULFID 66 104 BY SIMILARITY.

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FT DISULFID 73 97 BY SIMILARITY.
FT DISULFID 91 102 BY SIMILARITY.
FT METAL 43 43 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 45 45 (BY SIMILARITY).
FT METAL 47 47 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 47 47 (BY SIMILARITY).
FT METAL 64 64 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 64 64 (BY SIMILARITY).
SQ SEQUENCE 137 AA; 15309 MW; BDEC100B7F524431 CRC64;

Query Match 49.6%; Score 358; DB 1; Length 137;
Best Local Similarity 54.8%; Pred. No. 1e-31;
Matches 68; Conservative 11; Mismatches 41; Indels 4; Gaps 3;

QY 1 NLVQGVMIKMTGKSA-LQYNDYGCYCGIGSHWPVDQDWCHAHDCVGRLEKLGCE 59
DB 17 NLYQFGNMFQWTKSALLSYNVCYCGWGKGKGPQDADRCCFVHDCYGRV--GCD 74
QY 60 PKLEYLFSVSESGIFCAGRTTCORLTCECDKRAALCFRNLTGYNRYAHYPNKLTGP 119
DB 75 PKLSYSPENGDIVCGDDPCLRVCECDRAAICFGENLNTYDKKYNPSSHCT-E 133
QY 120 TPPC 123
DB 134 TEQC 137

RESULT 7
PA2_DABRR STANDARD; PRT; 121 AA.
AC PA2_DABRR STANDARD; PRT; 121 AA.
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Phospholipase A2 RVV-VD (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase).
DS Daboia russelli russelli (Russell's viper) (Vipera russelli russelli).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Daboia.
OC NCBI_TaxID=31159;
RN [1]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RC TISSUE=Venom;
RX MEDLINE=98267643; PubMed=9604284;
RA Carredano E., Westerlund B., Persson B., Saarinen M., Ramaswamy S.,
RA Eaker D., Eklund H.;
RT "The three-dimensional structures of two toxins from snake venom
RT throw light on the anticoagulant and neurotoxic sites of
RT phospholipase A2.";
RL Toxicon 36:75-92(1998).
CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides. This protein has anticoagulant activity.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a fatty acid anion.
CC -!- COFACTOR: Binds 1 calcium ion per subunit.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the phospholipase A2 family. Group II subfamily.
DR PDB; 1VIP; 16-JUN-97.
DR InterPro; IPR001211. PhospholipaseA2.
DR Pfam; PF00068; phoslip.
DR PRINTS; PR00389; PHPLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2c; 1.
DR PROSITE; PS00119; PA2_ASP; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
DR Hydrolase; Lipid degradation; Calcium; 3D-structure.
FT ACT_SITE 47 47
FT ACT_SITE 89 89

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FT DISULFID 26 115
FT DISULFID 28 44
FT DISULFID 43 95
FT DISULFID 49 121
FT DISULFID 50 88
FT DISULFID 57 81
FT DISULFID 75 86
FT METAL 27 27
FT METAL 29 29
FT METAL 31 31
FT METAL 48 48
FT HELIX 2 13
FT HELIX 17 20
FT STRAND 23 24
FT TURN 25 27
FT STRAND 28 29
FT HELIX 39 53
FT TURN 54 54
FT HELIX 55 57
FT TURN 59 61
FT STRAND 66 68
FT STRAND 73 75
FT HELIX 80 98
FT TURN 99 102
FT HELIX 105 107
FT STRAND 108 108
FT TURN 109 109
FT HELIX 112 114
SQ SEQUENCE 121 AA; 13626 MW; 98CBC4A8922A89D1 CRC64;

Query Match 49.2%; Score 355; DB 1; Length 121;
Best Local Similarity 53.2%; Pred. No. 1.9e-31;
Matches 66; Conservative 13; Mismatches 41; Indels 4; Gaps 3;

QY 1 NLVQGVMIKMTGKSA-LQYNDYGCYCGIGSHWPVDQDWCHAHDCVGRLEKLGCE 59
DB 1 NLQFAEIVMTGNPLSSSDYGCYCGWGKGKGPQDADRCCFVHDCYGRV--SCK 58
QY 60 PKLEYLFSVSESGIFCAGRTTCORLTCECDKRAALCFRNLTGYNRYAHYPNKLTGP 119
DB 59 PKLSYSPENGDIVCGDDPCLRVCECDRAAICFGENLNTYDKKYNPSSHCTG- 117
QY 120 TPPC 123
DB 118 TEQC 121

RESULT 8
PA21_AGKPI STANDARD; PRT; 123 AA.
ID PA21_AGKPI STANDARD; PRT; 123 AA.
AC PA21_AGKPI STANDARD; PRT; 123 AA.
DT 01-OCT-1996 (Rel. 34; Created)
DT 15-JUL-1998 (Rel. 36; Last sequence update)
DT 10-OCT-2003 (Rel. 42; Last annotation update)
DE Phospholipase A2 (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase) (APP-D-49).
OS Agkistrodon piscivorus piscivorus (Eastern cottonmouth).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Agkistrodon.
OC NCBI_TaxID=8716;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=93257049; PubMed=8489705;
RA Welches W., Reardon I.M., Heinrichson R.L.;
RT "An examination of structural interactions presumed to be of
RT importance in the stabilization of phospholipase A2 dimers based upon
RT comparative protein sequence analysis of a monomeric and dimeric
RT enzyme from the venom of Agkistrodon p. piscivorus.";

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RL J. Protein Chem. 12:187-193(1993).
RN [2]
RP SEQUENCE OF 1-23, AND ACYLATION.
RC TISSUE=Venom;
RX MEDLINE=88298768; PubMed=3403524;
RA Cho W., Tomasselli A.G., Heirlikson R.L., Kezdy F.J.;
RT "The chemical basis for interfacial activation of monomeric
RT phospholipases A2. Autocatalytic derivatization of the enzyme by acyl
RT transfer from substrate.";
RL J. Biol. Chem. 263:11237-11241(1988).
RN [3]
RP CHARACTERIZATION.
RC TISSUE=Venom;
RX MEDLINE=B5054816; PubMed=6438084;
RA Maraganore J.M., Merutka G., Cho W., Welches W., Kezdy F.J.,
RA Heirlikson R.L.;
RT "A new class of phospholipases A2 with lysine in place of aspartate
RT 49. Functional consequences for calcium and substrate binding.";
RL J. Biol. Chem. 259:13839-13843(1984).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
RC TISSUE=Venom;
RX MEDLINE=97166209; PubMed=9013608;
RA Han S.K., Yoon E.T., Scott D.L., Sigler P.B., Cho W.;
RT "Structural aspects of interfacial adsorption. A crystallographic and
RT site-directed mutagenesis study of the phospholipase A2 from the
RT venom of Agkistrodon piscivorus piscivorus.";
RL J. Biol. Chem. 272:3573-3582(1997).
RN [5]
RP FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
RP acyl groups in 3-sn-phosphoglycerides.
RC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
RC acylglycerophosphocholine + a fatty acid anion.
CC -1- COFACTOR: Binds 1 calcium ion per subunit.
CC -1- SUBUNIT: Monomer or homodimer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: Acylation causes dimerization.
CC -1- SIMILARITY: Belongs to the phospholipase A2 family. Group II
CC subfamily.
DR PIR; B53872; B53872.
DR PDB; 1VAP; 07-JUL-97.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PR00389; PHPLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2C; 1.
DR PROSITE; PS00119; PA2_ASP; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
KW Hydrolase; Lipid degradation; Calcium; Lipoprotein; Palmitate;
KW 3D-structure.
FT ACT_SITE 47 47
FT ACT_SITE 89 89 BY SIMILARITY.
FT ACT_SITE 26 116 BY SIMILARITY.
FT DISULFID 28 44
FT DISULFID 43 95
FT DISULFID 49 123
FT DISULFID 50 88
FT DISULFID 57 81
FT DISULFID 75 86
FT METAL 27 27 CALCIUM (VIA CARBONYL OXYGEN).
FT METAL 29 29 CALCIUM (VIA CARBONYL OXYGEN).
FT METAL 31 31 CALCIUM (VIA CARBONYL OXYGEN).
FT METAL 48 48 CALCIUM.
FT LIPID 7 7 N(6)-palmitoyl lysine.
FT LIPID 10 10 N(6)-palmitoyl lysine.
FT HELIX 2 13
FT HELIX 17 20
FT STRAND 23 24
FT TURN 25 27
FT STRAND 28 29
FT HELIX 39 52
FT TURN 53 53
FT TURN 59 61
FT STRAND 66 69

FT TURN 70 71
FT STRAND 72 75
FT HELIX 80 98
FT TURN 99 99
FT HELIX 100 102
FT HELIX 100 102
FT HELIX 105 108
FT STRAND 109 109
FT TURN 110 110
FT HELIX 113 116
SQ SEQUENCE 123 AA; 13989 MW; C39986552D990D72 CRC64;
Query Match 48.5%; Score 350; DB 1; Length 123;
Best Local Similarity 52.0%; Pred. No. 6.8e-31;
Matches 65; Conservative 14; Mismatches 42; Indels 4; Gaps 3;
QY 1 NLVQGVMLEKMTGKSA-LQYNDYCYGCGIGSHWPVDOTWCCHAHDCCYGRLEKGE 59
Db 1 NLFQFEKLIKMTGKSGMLWYSAYCYGCGWGQGPDKDTRCCFVHDCCKGV--TGCN 58
QY 60 PKLEKLYFSVSRGIFCAGRTTCQRLTCECDRAALCFERNLGTYNRK-YAHVPNKLCTG 118
Db 59 PRMDIYTVSDNGNIVCGTNPCKKQICECDRAAICFRDNLKTYDSKTYKPKKNCKE 118
QY 119 PTPPC 123
Db 119 ESEPC 123
RESULT 9
PA2A RAT STANDARD; PRT; 146 AA.
ID PA2A RAT
AC F14423;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Phospholipase A2, membrane associated precursor (EC 3.1.1.4)
DE (Phosphatidylcholine 2-acylhydrolase) (group IIA phospholipase A2)
DE (GIIC SPLA2).
GN PLA2G2A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Platelet;
RX MEDLINE=90110043; PubMed=2606907;
RA Komada M., Kudo I., Mizushima H., Kitamura N., Inoue K.;
RT "Structure of cDNA coding for rat platelet phospholipase A2.";
RL J. Biochem. 106:545-547(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=90267443; PubMed=2346480;
RA Komada M., Kudo I., Inoue K.;
RT "Structure of gene coding for rat group II phospholipase A2.";
RL Biochem. Biophys. Res. Commun. 168:1059-1065(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=89350908; PubMed=2764915;
RA Ishizaki J., Ohara O., Nakamura E., Tamaki M., Ono T., Kanda A.,
RA Yoshida N., Teraoka H., Tojo H., Okamoto M.;
RT "cDNA cloning and sequence determination of rat membrane-associated
RT phospholipase A2.";
RL Biochem. Biophys. Res. Commun. 162:1030-1036(1989).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=90381322; PubMed=2400792;
RA Kusunoki C., Satoh S., Kobayashi M., Niwa M.;
RT "Structure of genomic DNA for rat platelet phospholipase A2.";
RL Biochim. Biophys. Acta 1087:95-97(1990).
RN [5]

```

RP SEQUENCE OF 22-146.
RC STRAIN=Wistar; TISSUE=Platelet;
RX MEDLINE=89174508; PubMed=3235451;
RA Hayakawa M., Kudo I., Tomita M., Nojima S., Inoue K.;
RT "The primary structure of rat platelet phospholipase A2.";
RL J. Biochem. 104:767-772(1988).
RN [6]
RP SEQUENCE OF 22-57.
RC TISSUE=Spleen;
RX MEDLINE=86186890; PubMed=3356705;
RA Ono T., Tojo H., Kuramitsu S., Kagamiyama H., Okamoto M.;
RT "Purification and characterization of a membrane-associated
phospholipase A2 from rat spleen. Its comparison with a cytosolic
phospholipase A2 S-1.";
RL J. Biol. Chem. 263:5732-5738(1988).
RN [7]
RP SEQUENCE OF 22-46.
RC TISSUE=Platelet;
RX MEDLINE=88007474; PubMed=3654593;
RA Hayakawa M., Horigome K., Kudo I., Tomita M., Nojima S., Inoue K.;
RT "Amino acid composition and NH2-terminal amino acid sequence of rat
platelet secretory phospholipase A2.";
RL J. Biochem. 101:1311-1314(1987).
RN [8]
RP SEQUENCE OF 22-45.
RC TISSUE=Liver;
RX MEDLINE=89253484; PubMed=2722857;
RA Aarsman A.J., de Jong J.G.N., Arnoldussen E., Neys F.W.,
van Wassenaer P.D., van den Bosch H.;
RT "Immunocaffinity purification, partial
localization of rat liver phospholipase A2.";
RL J. Biol. Chem. 264:10008-10014(1989).
RN [9]
CC -!- FUNCTION: Thought to participate in the regulation of the
phospholipid metabolism in biomembranes including eicosanoid
biosynthesis. Catalyzes the calcium-dependent hydrolysis of the 2-
acyl groups in 3-sn-phosphoglycerides.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
acylglycerophosphocholine + a fatty acid anion.
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Membrane-associated.
CC -!- MISCELLANEOUS: Group II phospholipase A2 is found in many cells
and also extracellularly. The membrane-bound and secreted forms
are identical and are encoded by a single gene.
CC -!- SIMILARITY: Belongs to the phospholipase A2 family.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D00523; BAA0410.1; -
DR EMBL; M37127; AAA41223.1; -
DR EMBL; M25148; AAA41920.1; -
DR EMBL; X51529; CRA35909.1; -
DR PIR; A33394; A33394.
DR HSSP; P14555; 1P0D.
DR InterPro; IP0001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PK00389; PHPLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2G; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
DR PROSITE; PS00119; PA2_ASP; 1.
KW Hydrolase; Lipid degradation; Membrane; Signal; Calcium.
FT SIGNAL 1 21 PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED.
FT CHAIN 22 146 BY SIMILARITY.
FT ACT_SITE 68 68 BY SIMILARITY.
FT ACT_SITE 113 113 BY SIMILARITY.
FT DISULFID 47 139 BY SIMILARITY.
FT DISULFID 49 65 BY SIMILARITY.
FT -----

FT DISULFID 64 119 BY SIMILARITY.
FT DISULFID 70 146 BY SIMILARITY.
FT DISULFID 71 112 BY SIMILARITY.
FT DISULFID 80 105 BY SIMILARITY.
FT DISULFID 98 110 BY SIMILARITY.
FT METAL 48 48 CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
FT METAL 50 50 CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
FT METAL 52 52 CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
FT METAL 69 69 CALCIUM (BY SIMILARITY).
FT VARIANT 135 135 P -> L (POLYMORPHISM).
FT CONFLICT 22 22 S -> D (IN REF. 8).
FT CONFLICT 63 63 W -> E (IN REF. 5).
FT CONFLICT 69 69 D -> E (IN REF. 5).
FT CONFLICT 78 78 R -> S (IN REF. 5).
FT CONFLICT 85 85 L -> V (IN REF. 3).
FT CONFLICT 121 121 L -> S (IN REF. 5).
FT SEQUENCE 145 AA; 16294 MW; 60DDC9E79BF109F7 CRC64;
Query Match 48.1%; Score 347; DB 1; Length 146;
Best Local Similarity 51.2%; Pred. No. 1.7e-30;
Matches 64; Conservative 14; Mismatches 45; Indels 2; Gaps 2;

QY 1 NLVQFGVMIEKMTGKSA-LQYNDYCYGICGGSHWVPDQTDWCCHADCCYGRLEKLGCE 59
Db 22 SLLEFGQMLFKTKRADVSYGFYCHGCVGGRSPKDATDCCVTHDCCYNRLEKRGCG 81
QY 60 PKLEKYLFSVEERGIFCA-GRITQRLTCEDCKRAALCFRNLTGTYNKYAHYNNKLTGT 118
Db 82 TKFLTYKFSYRGQISCSSTNQDSCKQLCQCDKAAACFAFNKSKSYSLKYQFYFNKFKCG 141
QY 119 PTPPC 123
Db 142 KTPSC 146

RESULT 10
PA2Q TRIFL STANDARD; PRT; 138 AA.
ID PA2Q TRIFL STANDARD; PRT; 138 AA.
AC Q8JFGC;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Phospholipase A2 isozyme cPLA-B' (A) precursor (EC 3.1.1.4)
DE (Phosphatidylcholine 2-acylhydrolase).
OS Trimeresurus flavoviridis (Habu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OC NCBI_TaxID=8087;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=Amami-Oshima, and Kagosima; TISSUE=Venom gland;
RX MEDLINE=22499762; PubMed=1612832;
RA Chijiwa T., Yamaguchi Y., Ogawa I., Deshimaru M., Nobuhisa I.,
RA Nakashima K.-I., Oda-Ueda N., Fukumaki Y., Hattori S., Ono M.;
RT "Interisland evolution of Trimeresurus flavoviridis venom
phospholipase A(2) isozymes."
RL J. Mol. Evol. 56:286-293(2003).
CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the
-!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
acylglycerophosphocholine + a fatty acid anion.
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: Belongs to the phospholipase A2 family. Group II
subfamily.
CC -----
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EMBL; AB087496; BAC02719.1; -
InterPro; IPR001211; PhospholipaseA2.
Pfam; PF00068; phoslip; 1.
PRINTS; PR00389; PHPLIPASEA2.
ProDom; PD000303; PhospholipaseA2; 1.
SMART; SM00085; PA2C; 1.
PROSITE; PS00119; PA2_ASP; 1.
PROSITE; PS00118; PA2_HIS; 1.
Hydrolase; Lipid degradation; Calcium; Multigene family; Signal.
FT SIGNAL 1 16
FT CHAIN 17 138
FT ACT_SITE 63 63
FT ACT_SITE 105 105
FT DISULFID 42 131
FT DISULFID 44 60
FT DISULFID 59 111
FT DISULFID 65 104
FT DISULFID 66 104
FT DISULFID 73 97
FT DISULFID 91 102
FT METAL 43 43
FT METAL 45 45
FT METAL 47 47
FT METAL 64 64
FT METAL 64 64
SEQUENCE 138 AA; 15703 MW; CBDS40581DD2F10 CRC64;

Query Match 47.7%; Score 344.5; DB 1; Length 138;
Best Local Similarity 50.0%; Pred. No. 3e-30;
Matches 62; Conservative 15; Mismatches 44; Indels 3; Gaps 2;

QY 1 NLVQGVMIKMTGKSAI-QYNDYGCYGGSHWPVDQTDWCCHADCCYGRLEKLGCE 59
DB 17 HLLQFRMKIKMTGKEPIVSFAFYCYGCKGGRGPKDADRCCFVHDCYGVK--TGCD 74
QY 60 PKLEYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRYKHYPNKLTGTP 119
DB 75 PKWDYVYSSNGDIVCGDNPCTKEVCECDKAAAIACFRDNLKTYKRYMTFPDICTDP 134
QY 120 TPPC 123
DB 135 TEKC 138

RESULT 11
PA2Y_TRIFL STANDARD; PRT; 138 AA.
AC Q90Y77;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Phospholipase A2 isozyme PL-Y precursor (EC 3.1.1.4)
DE (Phosphatidylcholine 2-acylhydrolase).
OS Trimeresurus flavoviridis (Habu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=88087;
RN [1]
RP SEQUENCE FROM N.A.
RA Chjiwa T., Yamaguchi Y., Ogawa T., Deshimaru M., Nobuhisa I.,
RA Nakashima K.-I., Oda-Ueda N., Shimohigashi Y., Fukumaki Y.,
RA Hattori S., Ohno M.,
RT "Regional evolution of Trimeresurus flavoviridis venom-gland phospholipase A2 isozymes.";

Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides (By similarity).
-!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a fatty acid anion.
-!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
-!- SUBCELLULAR LOCATION: Secreted (By similarity).
-!- TISSUE SPECIFICITY: Expressed by the venom gland (Probable).
-!- SIMILARITY: Belongs to the phospholipase A2 family. Group II subfamily.

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EMBL; AB072173; BAB68546.1; -
InterPro; IPR001211; PhospholipaseA2.
Pfam; PF00068; phoslip; 1.
PRINTS; PR00389; PHPLIPASEA2.
ProDom; PD000303; PhospholipaseA2; 1.
SMART; SM00085; PA2C; 1.
PROSITE; PS00119; PA2_ASP; 1.
PROSITE; PS00118; PA2_HIS; 1.
Hydrolase; Lipid degradation; Calcium; Multigene family; Signal.
FT SIGNAL 1 16
FT CHAIN 17 138
FT ACT_SITE 63 63
FT ACT_SITE 105 105
FT DISULFID 42 131
FT DISULFID 44 60
FT DISULFID 59 111
FT DISULFID 65 138
FT DISULFID 66 104
FT DISULFID 73 97
FT DISULFID 91 102
FT METAL 43 43
FT METAL 45 45
FT METAL 47 47
FT METAL 64 64
FT METAL 64 64
SEQUENCE 138 AA; 15729 MW; C96B1B878CCAL196 CRC64;

Query Match 47.7%; Score 344.5; DB 1; Length 138;
Best Local Similarity 49.2%; Pred. No. 3e-30;
Matches 61; Conservative 17; Mismatches 43; Indels 3; Gaps 2;

QY 1 NLVQGVMIKMTGKSAI-QYNDYGCYGGSHWPVDQTDWCCHADCCYGRLEKLGCE 59
DB 17 HLLQFRMKIKMTGKEPIVSFAFYCYGCKGGRGPKDADRCCFVHDCYGVK--TGCD 74
QY 60 PKLEYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRYKHYPNKLTGTP 119
DB 75 PKWDYVYSSNGDIVCGDNPCTKEVCECDKAAAIACFRDNLKTYKRYMTFPDICTDP 134
QY 120 TPPC 123
DB 135 TEKC 138

RESULT 12
PA2A_MOUSE STANDARD; PRT; 146 AA.
ID PA2A_MOUSE
AC F31482; Q60871;
DT 01-JUL-1993 (Rel. 26, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Phospholipase A2, membrane associated precursor (EC 3.1.1.4)

DE (Phosphatidylcholine 2'-acylhydrolase) (Group IIA phospholipase A2)
 DE (Gric sPLA2) (Enhancing factor) (EF).
 OS PLA2G2A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/c;
 RA Mulherkar R.;
 RN Submitted (OCT-1994) to the EMBL/GenBank/DBSJ databases.
 [2]
 RP SEQUENCE FROM N.A., AND POLYMORPHISM.
 RC STRAIN=BALE/c, and CD-1, TISSUE=Intestine;
 RX MEDLINE=9403435; PubMed=7673223;
 RA Kennedy B.P., Payette P., Mudgett J., Vadas P., Pruzanski W.,
 RA Yvan M., Tang C., Rancourt D.E., Cromlish W.;
 RT "A natural disruption of the secretory group II phospholipase A2 gene
 in inbred mouse strains.";
 RL J. Biol. Chem. 270:22378-22385(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H;
 RX MEDLINE=95300227; PubMed=7781071;
 RA MacPhee M., Chepenik K.P., Liddell R.A., Nelson K.K., Siracusa L.D.,
 RA Buchpree A.M.;
 RT "The secretory phospholipase A2 gene is a candidate for the Mom1
 locus, a major modifier of ApcMin-induced intestinal neoplasia.";
 RL Cell 81:957-966(1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Richards S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.N., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 22-146 FROM N.A.
 RC STRAIN=BALE/c; TISSUE=Small intestine;
 RX MEDLINE=94029555; PubMed=8267767;
 RA Mulherkar R., Rao R.S., Wagie A.S., Patki V., Deo M.G.;
 RT "Enhancing factor, a Paneth cell specific protein from mouse small
 intestines: predicted amino acid sequence from RT-PCR amplified cDNA
 and its expression.";
 RL Biochem. Biophys. Res. Commun. 195:1254-1263(1993).
 RN [6]
 RP ERRATUM.
 RX MEDLINE=94071967; PubMed=8250944;
 RA Mulherkar R., Rao R.S., Wagie A.S., Patki V., Deo M.G.;
 RL Biochem. Biophys. Res. Commun. 197:351-352(1993).
 RN [7]
 RP PRELIMINARY SEQUENCE OF 22-41.
 RC TISSUE=Small intestine;
 RX MEDLINE=93146172; PubMed=8425615;
 RA Mulherkar R., Rao R., Rao L., Patki V., Chauhan V.S., Deo M.G.;

RT "Enhancing factor protein from mouse small intestines belongs to the
 RT phospholipase A2 family.";
 RL FEBS Lett. 317:263-266(1993).
 CC -!- FUNCTION: May play a role in cell proliferation, by increasing the
 CC binding of EGF to the cells and thereby modulating its action. In
 CC doing so, this isozyme binds to a membrane-associated receptor
 CC distinct from the EGF receptor and which could be a heparan-
 CC sulfate proteoglycan located on the cell membrane.
 CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
 CC acyl groups in 3-sn-phosphoglycerides.
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a fatty acid anion.
 CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
 CC -!- SUBCELLULAR LOCATION: Membrane-associated.
 CC -!- TISSUE SPECIFICITY: Mainly in the Paneth cells adjacent to the
 CC stem population in the small intestines. Also expressed in
 CC regenerating liver and hyperplastic esophageal epithelium.
 CC -!- POLYMORPHISM: In strains 129/Sv, B10.RIII and C57BL/6, a
 CC polymorphism causes a frameshift and premature truncation of the
 CC protein, rendering it inactive. Strains BALB/c, C3H/He, DBA/1,
 CC DBA/2, MRL and NZB/B1N contain the normal protein while strain CD-
 CC 1 is heterozygous for the mutation.
 CC -!- SIMILARITY: Belongs to the phospholipase A2 family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X74266; CAA52325.1; -.
 CC EMBL: U32358; AAC52252.1; -.
 CC EMBL: U28244; AAB06315.1; ALT INIT.
 CC EMBL: BC045156; AAH45156.1; -.
 CC PIR: I48342; I48342.
 CC PIR: S29495; S29495.
 CC HSSP: P14555; IPOB.
 CC MGD: MG1:104642; Pla2g2a.
 CC InterPro: IPR001211; PhospholipaseA2.
 CC Pfam: PF00068; phoslip; 1.
 CC PRINTS: PR00389; PHPLIPAS2A2.
 CC ProDom: PD000303; PhospholipaseA2; 1.
 CC SMART: SM00085; PA2C; 1.
 CC PROSITE: PS00118; PA2_HIS; 1.
 CC PROSITE: PS00119; PA2_ASP; 1.
 CC Hydrolase; Lipid degradation; Calcium; Growth regulation; Signal;
 KW Membrane; Polymorphism.
 FT SIGNAL 1 21
 FT CHAIN 22 146 PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED.
 FT ACT_SITE 68 68 BY SIMILARITY.
 FT ACT_SITE 113 113 BY SIMILARITY.
 FT DISULFID 47 139 BY SIMILARITY.
 FT DISULFID 49 65 BY SIMILARITY.
 FT DISULFID 64 119 BY SIMILARITY.
 FT DISULFID 70 146 BY SIMILARITY.
 FT DISULFID 71 112 BY SIMILARITY.
 FT DISULFID 80 105 BY SIMILARITY.
 FT DISULFID 98 110 BY SIMILARITY.
 FT METAL 48 48 CALCIUM (VIA CARBONYL OXYGEN)
 FT METAL 50 50 (BY SIMILARITY).
 FT METAL 52 52 CALCIUM (VIA CARBONYL OXYGEN)
 FT METAL 52 52 (BY SIMILARITY).
 FT METAL 69 69 CALCIUM (VIA CARBONYL OXYGEN)
 FT CONFLICT 19 19 V -> D (IN REF. 1).
 FT CONFLICT 86 86 K -> T (IN REF. 1).
 SQ SEQUENCE 146 AA; 16145 MW; AB304F6B3B1BA5C7 CRC64;
 Query Match 47.2%; Score 341; DB 1; Length 146;
 Best Local Similarity 52.8%; Pred. No. 7.6e-30;


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FT DISULFID 74 85 BY SIMILARITY.
FT METAL 26 26 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 28 28 (BY SIMILARITY).
FT METAL 28 28 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 30 30 (BY SIMILARITY).
FT METAL 30 30 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 47 47 (BY SIMILARITY).
FT METAL 47 47 CALCIUM (BY SIMILARITY).
SQ SEQUENCE 121 AA; 13363 MW; DC0500A87839E504 CRC64;

Query Match 47.1%; Score 340; DB 1; Length 121;
Best Local Similarity 47.2%; Pred. No. 8e-30;
Matches 58; Conservative 15; Mismatches 48; Indels 2; Gaps 1;

QY 1 NLVQGVMIKMTGKSLQYNDYCYGIGSGHWPVDQWCHAHDCCYGRLEKLGCEP 60
DB 1 NLVQGVMIKMTGKSLQYNDYCYGIGSGHWPVDQWCHAHDCCYGRLEKLGCEP 58
QY 61 KLEYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFERNLGTYNRYAHYPNKLCTGPT 120
DB 59 KMILYSYKFNHNGVCGDKNACKKKVCECDRVAALCFPAASKHSYKULWRYPPSSKCTGTA 118
QY 121 PPC 123
DB 119 EKC 121

RESULT 15
PA2X_TRIFL STANDARD; PRT; 122 AA.
ID PA2X_TRIFL STANDARD; PRT; 122 AA.
AC P06860;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Phospholipase A2 isozyme PL-X (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase).
OS Trimeresurus flavoviridis (Habu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=88087;
RN [1]
RP SEQUENCE.
RC TISSUE=venom;
RX MEDLINE=87179112; PubMed=3564060;
RA Kiri R.M., Kawabata S.-I., Iwanaga S.;
RT "Comparison of amino terminal region of three isoenzymes of phospholipases A2 (TFV PL-Ia, TFV PL-Ib, TFV PL-X) from Trimeresurus flavoviridis (habu snake) venom and the complete amino acid sequence of the basic phospholipase, TFV PL-X.";
RL Toxicon 24:1117-1129(1986).
CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a fatty acid anion.
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: Belongs to the phospholipase A2 family. Group II subfamily.
DR PIR; A25500; PSTVXF.
DR HSSP; P51972; 1VAP.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PR00389; PHEPLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2C; 1.
DR PROSITE; PS00119; PA2_ASP; FALSE_NEG.
DR PROSITE; PS00118; PA2_HIS; 1.
KW Hydrolase; Lipid degradation; Calcium; Multigene family.
FT ACT_SITE 47 47 BY SIMILARITY.
FT ACT_SITE 89 89 BY SIMILARITY.
FT DISULFID 26 115 BY SIMILARITY.

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FT DISULFID 28 44 BY SIMILARITY.
FT DISULFID 43 95 BY SIMILARITY.
FT DISULFID 49 122 BY SIMILARITY.
FT DISULFID 50 88 BY SIMILARITY.
FT DISULFID 57 81 BY SIMILARITY.
FT DISULFID 75 86 BY SIMILARITY.
FT METAL 27 27 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 29 29 (BY SIMILARITY).
FT METAL 29 29 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 31 31 (BY SIMILARITY).
FT METAL 31 31 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 48 48 (BY SIMILARITY).
FT METAL 48 48 CALCIUM (BY SIMILARITY).
SQ SEQUENCE 122 AA; 13981 MW; A9D652276C5D0DF0 CRC64;

Query Match 47.0%; Score 339.5; DB 1; Length 122;
Best Local Similarity 49.2%; Pred. No. 9.2e-30;
Matches 61; Conservative 16; Mismatches 44; Indels 3; Gaps 2;

QY 1 NLVQGVMIKMTGKSLQYNDYCYGIGSGHWPVDQWCHAHDCCYGRLEKLGCEP 59
DB 1 HLQPRKMIKMTGKEPIVSVAFYCYCGKGRGPKDADRCCFVHDCCYEKV--TGCD 58
QY 60 PKLEYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFERNLGTYNRYAHYPNKLCTGP 119
DB 59 PKMSYTYTSLENGDIVCGDPYCTKVKCECDKRAALCFERNLGTYNRYAHYPNKLCTGP 118
QY 120 TPPC 123
DB 119 TEGC 122

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Search completed: July 3, 2004, 05:16:40
Job time : 9.81887 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2004, 05:15:00 ; Search time 12.5321 Seconds
(without alignments)
506.699 Million cell updates/sec

Title: US-10-088-092A-30_COPY_20_142

Perfect score: 722

Sequence: 1 NLVQFGVMEKMTGKALQY.....YNRKVAHYENKLTGTPPTPC 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
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5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	360.5	49.9	124	1	US-08-170-360-4
2	360.5	49.9	124	2	US-08-888-497-39
3	360.5	49.9	124	4	US-09-362-230-39
4	360.5	49.9	124	4	US-09-740-569-2
5	360.5	49.9	124	5	PCT-US94-07926-39
6	360.5	49.9	144	1	US-08-186-895-10
7	360.5	49.9	144	2	US-08-888-497-37
8	360.5	49.9	144	4	US-09-362-230-37
9	360.5	49.9	144	5	PCT-US94-07926-37
10	348	48.2	125	2	US-08-888-497-42
11	348	48.2	125	4	US-09-362-230-42
12	348	48.2	125	5	PCT-US94-07926-42
13	348	48.2	146	2	US-08-888-497-35
14	348	48.2	146	4	US-09-362-230-35
15	348	48.2	146	5	PCT-US94-07926-35
16	341	47.2	146	3	US-08-966-317-3
17	341	47.2	146	4	US-09-489-770-3
18	337	46.7	146	3	US-08-966-317-4
19	337	46.7	146	4	US-09-489-770-4
20	321	44.5	125	1	US-08-170-360-5
21	299.5	41.5	118	2	US-08-888-497-40
22	299.5	41.5	118	4	US-09-097-094-5
23	299.5	41.5	118	5	US-09-362-230-40
24	299.5	41.5	118	5	PCT-US94-07926-40
25	299.5	41.5	122	1	US-07-734-534A-1
26	299.5	41.5	138	2	US-08-888-497-32
27	299.5	41.5	138	4	US-09-362-230-32

28	299.5	41.5	138	5	PCT-US94-07926-32
29	296.5	41.1	117	2	US-08-888-497-44
30	296.5	41.1	117	4	US-09-362-230-44
31	296.5	41.1	117	5	PCT-US94-07926-44
32	296.5	41.1	137	2	US-08-888-497-30
33	296.5	41.1	137	4	US-09-362-230-30
34	296.5	41.1	137	5	PCT-US94-07926-30
35	287.5	39.8	165	3	US-08-966-317-1
36	287.5	39.8	165	4	US-09-489-770-1
37	286	39.6	130	2	US-08-888-497-43
38	286	39.6	130	4	US-09-362-230-43
39	286	39.6	130	5	PCT-US94-07926-43
40	286	39.6	158	2	US-08-888-497-22
41	286	39.6	158	4	US-09-362-230-22
42	286	39.6	158	5	PCT-US94-07926-22
43	244	33.8	118	3	US-09-090-602-4
44	226.5	31.4	126	1	US-08-170-360-3
45	226.5	31.4	126	2	US-08-888-497-38

ALIGNMENTS

RESULT 1
US-08-170-360-4
; Sequence 4, Application US/08170360
; Patent No. 5656602
; GENERAL INFORMATION:
; APPLICANT: Tseng, Albert P. S.
; APPLICANT: Ingllis, Adam
; TITLE OF INVENTION: PLA2 INHIBITORY COMPOUNDS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Perry Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20004

1997 (issued)

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/170,360
FILING DATE: 03-MAR-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PCT/AU92/00333
FILING DATE: 06-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK 7058
FILING DATE: 04-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Ernst, Barbara G.
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1871-104A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)783-6040
TELEFAX: (202)783-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-170-360-4

Query Match 49.9%; Score 360.5; DB 1; Length 124;
Best Local Similarity 55.6%; Pred. No. 1.3e-31;
Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;
QY 1 NLVFGVMIERMTGK-SALQYNDYGCYGGSHWPVDQTDWCHADCCYGRLEKLGCE 59
DB 1 NLVFNHRMIKLTGTGKAALSYGFYCHGCGVGRGSPKDATDRCCVTHDCCYKLEKRGCG 60
QY 60 PKLEKYLFSVSERGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRYAHYPNKLCTGP 119
DB 61 TKFLSYKFSNGSRITCAKQDSCRSQCECDKAAATCFARNKTTYNKYQYYSNKHCRGS 120
QY 120 TTPC 123
DB 121 TPRC 124

RESULT 2

US-08-888-497-39
; Sequence 39, Application US/08888497
; Patent No. 5972677
; GENERAL INFORMATION:
; APPLICANT: Tischerfeld, Jay A.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,497
; FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/651,405
FILING DATE:
APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-888-497-39

Query Match 49.9%; Score 360.5; DB 2; Length 124;
Best Local Similarity 55.6%; Pred. No. 1.3e-31;
Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;
QY 1 NLVFGVMIERMTGK-SALQYNDYGCYGGSHWPVDQTDWCHADCCYGRLEKLGCE 59
DB 1 NLVFNHRMIKLTGTGKAALSYGFYCHGCGVGRGSPKDATDRCCVTHDCCYKLEKRGCG 60
QY 60 PKLEKYLFSVSERGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRYAHYPNKLCTGP 119
DB 61 TKFLSYKFSNGSRITCAKQDSCRSQCECDKAAATCFARNKTTYNKYQYYSNKHCRGS 120

DB 1 NLVFNHRMIKLTGTGKAALSYGFYCHGCGVGRGSPKDATDRCCVTHDCCYKLEKRGCG 60
QY 60 PKLEKYLFSVSERGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRYAHYPNKLCTGP 119
DB 61 TKFLSYKFSNGSRITCAKQDSCRSQCECDKAAATCFARNKTTYNKYQYYSNKHCRGS 120
QY 120 TTPC 123
DB 121 TPRC 124

RESULT 3

US-09-362-230-39
; Sequence 39, Application US/09362230
; Patent No. 6352849
; GENERAL INFORMATION:
; APPLICANT: Tischerfeld, Jay A.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/362,230
; FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/888,497
FILING DATE:
APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-362-230-39

Query Match 49.9%; Score 360.5; DB 4; Length 124;
Best Local Similarity 55.6%; Pred. No. 1.3e-31;
Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;
QY 1 NLVFGVMIERMTGK-SALQYNDYGCYGGSHWPVDQTDWCHADCCYGRLEKLGCE 59
DB 1 NLVFNHRMIKLTGTGKAALSYGFYCHGCGVGRGSPKDATDRCCVTHDCCYKLEKRGCG 60
QY 60 PKLEKYLFSVSERGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRYAHYPNKLCTGP 119
DB 61 TKFLSYKFSNGSRITCAKQDSCRSQCECDKAAATCFARNKTTYNKYQYYSNKHCRGS 120

QY 120 TPPC 123
Db 121 TPRC 124

RESULT 4

US-09-740-569-2
; Sequence 2, Application US/09740569
; Patent No. 6475484
; GENERAL INFORMATION:
; APPLICANT: Weiss, Jerrold
; APPLICANT: Elsbach, Peter
; APPLICANT: Liang, Ning-Sheng
; TITLE OF INVENTION: ANTIBACTERIAL GROUP IIA PHOSPHOLIPASE A2 AND METHODS OF USE THERE
; FILE REFERENCE: 5986/1E917US1
; CURRENT APPLICATION NUMBER: US/09/740,569
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/172,467
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-740-569-2

Query Match 49.9%; Score 360.5; DB 4; Length 124;
Best Local Similarity 54.8%; Pred. No. 1.3e-31;
Matches 68; Conservative 11; Mismatches 44; Indels 1; Gaps 1;

QY 1 NLVQFGVMIEKMTGK-SALQYNDYGCYGGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE 59
Db 1 NLVNFHRLIKLTGKEAALSFGYCHGCVGRGSPKDATDCCVTHDCCYKLEKRGCG 60
QY 60 PLEKYLFSVSRGIFCAGRTTCORLTCECDKRAALCFRRNLGTYNRKVAHYPNKLCCTGP 119
Db 61 TKLSYKFSNKSRIITCAKQDSQSCSLCECDKAAATCFARNKTYNKKYQYYSNKHCRGS 120
QY 120 TPPC 123
Db 121 TPRC 124

RESULT 5

PCT-US94-07926-39
; Sequence 39, Application PC/TUS9407926
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07926
; FILING DATE: 15-JUL-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/097,354
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-07926-39

Query Match 49.9%; Score 360.5; DB 5; Length 124;
Best Local Similarity 55.6%; Pred. No. 1.3e-31;
Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;

QY 1 NLVQFGVMIEKMTGK-SALQYNDYGCYGGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE 59
Db 1 NLVNFHRLIKLTGKEAALSFGYCHGCVGRGSPKDATDCCVTHDCCYKLEKRGCG 60
QY 60 PLEKYLFSVSRGIFCAGRTTCORLTCECDKRAALCFRRNLGTYNRKVAHYPNKLCCTGP 119
Db 61 TKLSYKFSNKSRIITCAKQDSQSCSLCECDKAAATCFARNKTYNKKYQYYSNKHCRGS 120
QY 120 TPPC 123
Db 121 TPRC 124

RESULT 6

US-08-186-895-10
; Sequence 10, Application US/08186895
; Patent No. 5538885
; GENERAL INFORMATION:
; APPLICANT: Hollis, Melvyn
; APPLICANT: Needham, Maurice R.C.
; APPLICANT: Gooding, Clare
; APPLICANT: Grosveld, Franklin G.
; TITLE OF INVENTION: Expression Systems
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cushman, Darby & Cushman
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,895
; FILING DATE: 27-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/046,383
; FILING DATE: 09-APR-1993
; APPLICATION NUMBER: US/07/810,414
; ATTORNEY/AGENT INFORMATION:
; NAME: Kokulis, Paul N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: PNK/3893/93802/MJW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944

4

[illegible]

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/097,354
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-07926-35

Query Match      48.2%; Score 348; DB 5; Length 146;
Best Local Similarity 51.2%; Pred. No. 3.5e-30;
Matches 64; Conservative 14; Mismatches 45; Indels 2; Gaps 2;

Qy      1 NLVQFGWMIKMTGKSA-LQNDYGCYCGIGSHWPVDQTDWCCHADCCYGRLEKLGCE 59
Db      22 SLLEFGQMILFKTKGRADVSYGFYCHGCVGGSGSPKDATDWCCVTHDCCYNLEKRGCG 81
Qy      60 PKLEKYLFSVSERGIFCA-GRITTCQRLTCECDKRAALCFRRNLGTYNRYAHYPNKLCTG 118
Db      82 TKFVTKESYRGQISCSSTNQDSCEKQLCCDRAAECPARNKKSYSLSKYQFYFNKECKG 141
Qy      119 FPPPC 123
Db      142 KTPSC 146
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Search completed: July 3, 2004, 05:18:47
Job time : 13.5321 secs